

Ile Pro His Glu Asn Gly Val His Ser Ile Asp Val Lys Phe Asn Gly
 2450 2455 2460
 Ala His Ile Pro Gly Ser Pro Phe Lys Ile Arg Val Gly Glu Gln Ser
 2465 2470 2475 2480
 Gln Ala Gly Asp Pro Gly Leu Val Ser Ala Tyr Gly Pro Gly Leu Glu
 2485 2490 2495
 Gly Gly Thr Thr Gly Val Ser Ser Glu Phe Ile Val Asn Thr Leu Asn
 2500 2505 2510
 Ala Gly Ser Gly Ala Leu Ser Val Thr Ile Asp Gly Pro Ser Lys Val
 2515 2520 2525
 Gln Leu Asp Cys Arg Glu Cys Pro Glu Gly His Val Val Thr Tyr Thr
 2530 2535 2540
 Pro Met Ala Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro
 2545 2550 2555 2560
 Gln His Ile Val Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg
 2565 2570 2575
 Leu Ser Gly Gly His Ser Leu His Glu Thr Ser Thr Val Leu Val Glu
 2580 2585 2590
 Thr Val Thr Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile
 2595 2600 2605
 Pro Lys Phe Ser Ser Asp Ala Ser Lys Val Val Thr Arg Gly Pro Gly
 2610 2615 2620
 Leu Ser Gln Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys
 2625 2630 2635 2640
 Ser Lys Ala Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys
 2645 2650 2655
 Thr Pro Cys Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr

2660 2665 2670
 Asn Val Thr Tyr Thr Val Lys Glu Lys Gly Asp Tyr Ile Leu Ile Val

2675 2680 2685
 Lys Trp Gly Asp Glu Ser Val Pro Gly Ser Pro Phe Lys Val Lys Val

2690 2695 2700
 Pro

2705

<210> 45

<211> 2016

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210).. (1352)

<400> 45

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 gaccccgctg cgcacggcct gtcgcctgca caccagcttg ttggcgcttt cgtcgccgcg 180
 ctcgcgcgcg gctactctg cgcgcgcaca atg agc tcc cgc atc gcc agg gcg 233

Met Ser Ser Arg Ile Ala Arg Ala

1

5

ctc gcc tta gtc gtc acc ctt ctc cac ttg acc agg ctg gcg ctc tcc 281

Leu Ala Leu Val Val Thr Leu Leu His Leu Thr Arg Leu Ala Leu Ser

10

15

20

acc tgc ccc gct gcc tgc cac tgc ccc ctg gag gcg ccc aag tgc gcg 329

Thr Cys Pro Ala Ala Cys His Cys Pro Leu Glu Ala Pro Lys Cys Ala

25	30	35	40	
ccg gga gtc ggg ctg gtc cgg gac ggc tgc ggc tgc tgt aag gtc tgc	377			
Pro Gly Val Gly Leu Val Arg Asp Gly Cys Gly Cys Cys Lys Val Cys				
45	50	55		
gcc aag cag ctc aac gag gac tgc agc aaa acg cag ccc tgc gac cac	425			
Ala Lys Gln Leu Asn Glu Asp Cys Ser Lys Thr Gln Pro Cys Asp His				
60	65	70		
acc aag ggg ctg gaa tgc aac ttc ggc gcc agc tcc acc gct ctg aag	473			
Thr Lys Gly Leu Glu Cys Asn Phe Gly Ala Ser Ser Thr Ala Leu Lys				
75	80	85		
ggg atc tgc aga gct cag tca gag ggc aga ccc tgt gaa tat aac tcc	521			
Gly Ile Cys Arg Ala Gln Ser Glu Gly Arg Pro Cys Glu Tyr Asn Ser				
90	95	100		
aga atc tac caa aac ggg gaa agt ttc cag ccc aac tgt aaa cat cag	569			
Arg Ile Tyr Gln Asn Gly Glu Ser Phe Gln Pro Asn Cys Lys His Gln				
105	110	115	120	
tgc aca tgt att gat ggc gcc gtg ggc tgc att cct ctg tgt ccc caa	617			
Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Ile Pro Leu Cys Pro Gln				
125	130	135		
gaa cta tct ctc ccc aac ttg ggc tgt ccc aac cct cgg ctg gtc aaa	665			
Glu Leu Ser Leu Pro Asn Leu Gly Cys Pro Asn Pro Arg Leu Val Lys				
140	145	150		
gtt acc ggg cag tgc tgc gag gag tgg gtc tgt gac gag gat agt atc	713			
Val Thr Gly Gln Cys Cys Glu Glu Trp Val Cys Asp Glu Asp Ser Ile				
155	160	165		
aag gac ccc atg gag gac cag gac ggc ctc ctt ggc aag gag ctg gga	761			

Lys Asp Pro Met Glu Asp Gln Asp Gly Leu Leu Gly Lys Glu Leu Gly
 170 175 180
 ttc gat gcc tcc gag gtg gag ttg acg aga aac aat gaa ttg att gca 809
 Phe Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn Glu Leu Ile Ala
 185 190 195 200
 gtt gga aaa ggc agc tca ctg aag cgg ctc cct gtt ttt gga atg gag 857
 Val Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val Phe Gly Met Glu
 205 210 215
 cct cgc atc cta tac aac cct tta caa ggc cag aaa tgt att gtt caa 905
 Pro Arg Ile Leu Tyr Asn Pro Leu Gln Gly Gln Lys Cys Ile Val Gln
 220 225 230
 aca act tca tgg tcc cag tgc tca aag acc tgt gga act ggt atc tcc 953
 Thr Thr Ser Trp Ser Gln Cys Ser Lys Thr Cys Gly Thr Gly Ile Ser
 235 240 245
 aca cga gtt acc aat gac aac cct gag tgc cgc ctt gtg aaa gaa acc 1001
 Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys Glu Thr
 250 255 260
 cgg att tgt gag gtg cgg cct tgt gga cag cca gtg tac agc agc ctg 1049
 Arg Ile Cys Glu Val Arg Pro Cys Gly Gln Pro Val Tyr Ser Ser Leu
 265 270 275 280
 aaa aag ggc aag aaa tgc agc aag acc aag aaa tcc ccc gaa cca gtc 1097
 Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys Lys Ser Pro Glu Pro Val
 285 290 295
 agg ttt act tac gct gga tgt ttg agt gtg aag aaa tac cgg ccc aag 1145
 Arg Phe Thr Tyr Ala Gly Cys Leu Ser Val Lys Lys Tyr Arg Pro Lys
 300 305 310
 tac tgc ggt tcc tgc gtg gac ggc cga tgc tgc acg ccc cag ctg acc 1193

Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Gln Leu Thr

315

320

325

agg act gtc aag atg cgg ttc cgc tgc gaa gat ggg gag aca ttt tcc 1241

Arg Thr Val Lys Met Arg Phe Arg Cys Glu Asp Gly Glu Thr Phe Ser

330

335

340

aag aac gtc atg atg atc cag tcc tgc aaa tgc aac tac aac tgc ccg 1289

Lys Asn Val Met Met Ile Gln Ser Cys Lys Cys Asn Tyr Asn Cys Pro

345

350

355

360

cat gcc aat gaa gca gcg ttt ccc ttc tac agg ctg ttc aat gac att 1337

His Ala Asn Glu Ala Ala Phe Pro Phe Tyr Arg Leu Phe Asn Asp Ile

365

370

375

cac aaa ttt agg gac taaatgctac ctgggtttcc agggcacacc tagacaaaca 1392

His Lys Phe Arg Asp

380

agggagaaga gtgtcagaat cagaatcatg gagaaaatgg gcgggggltgg tgtgggtgat 1452

gggactcatt glagaaagga agccttgctc attcttgagg agcattaaagg tatttcgaaa 1512

ctgccaaggg tgctggtgcg gatggacact aatgcagcca cgattggaga atactttgct 1572

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ctltgacaaa agtaaatggg agggcattcc atcccttcct gaagggggac actccatgag 1812

tgtctgtgag aggcagctat ctgcactctc aactgcaaac agaaatcagg tgttttaaga 1872

ctgaatgttt tatttatcaa aatgtagctt ttggggaggg aggggaaatg taatactgga 1932

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catttaataa agaaatatatt acct 2016

<211> 381

<212> PRT

<213> Homo sapiens

<400> 46

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20 25 30

Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp

35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys

50 55 60

Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe

65 70 75 80

Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu

85 90 95

Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser

100 105 110

Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val

115 120 125

Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly

130 135 140

Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu

145 150 155 160

Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp

165 170 175

Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
 180 185 190
 Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Ser Ser Leu Lys
 195 200 205
 Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
 210 215 220
 Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
 225 230 235 240
 Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro
 245 250 255
 Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
 260 265 270
 Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys
 275 280 285
 Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu
 290 295 300
 Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly
 305 310 315 320
 Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg
 325 330 335
 Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser
 340 345 350
 Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro
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 Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
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<210> 47

<211> 2743

<212> DNA

<213> Homo sapiens

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<222> (240).. (2387)

<400> 47

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cgcgcgggcg tgagccccggg gcgagggtcg tcttcccgga gaccgaccc cggcagcgcg 180
ggcgggccac ttctcctgig cctccgcccc ctgctccact ccccgccgcc gccgcgcgg 239
atg cca agc acc agc ttt cca gtc cct tcc aag ttt cca ctt ggc cct 287
Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro
      1           5           10           15
gcg gct gcg gtc ttc ggg aga gga gaa act ttg ggg ccc gcg ccg cgc 335
Ala Ala Ala Val Phe Gly Arg Gly Glu Thr Leu Gly Pro Ala Pro Arg
           20           25           30
gcc ggc ggc acc atg aag tca gcg gag gaa gaa cac tat ggc tat gca 383
Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala
           35           40           45
tcc tcc aac gtc agc ccc gcc ctg ccg ctg ccc acg gcg cac tcc acc 431
Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr
           50           55           60
ctg ccg gcc ccg tgc cac aac ctt cag acc tcc aca ccg ggc atc atc 479
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile
           65           70           75           80

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ccg ccg gcg gat cac ccc tcg ggg tac gga gca gct ttg gac ggt ggg	527
Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly	
85 90 95	
ccc gcg ggc tac ttc ctc tcc tcc ggc cac acc agg cct gat ggg gcc	575
Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala	
100 105 110	
cct gcc ctg gag agt cct cgc atc gag ata acc tcg tgc ttg ggc ctg	623
Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu	
115 120 125	
tac cac aac aal aac cag ttt ttc cac gat gtg gag gtg gaa gac gtc	671
Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val	
130 135 140	
ctc cct agc tcc aaa cgg tcc ccc tcc acg gcc acg ctg agt ctg ccc	719
Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro	
145 150 155 160	
agc ctg gag gcc tac aga gac ccc tcg tgc ctg agc ccg gcc agc agc	767
Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser	
165 170 175	
ctg tcc tcc cgg agc tgc aac tca gag gcc tcc tcc tac gag tcc aac	815
Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn	
180 185 190	
tac tcg tac ccg tac gcg tcc ccc cag acg tcg cca tgg cag tct ccc	863
Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro	
195 200 205	
tgc gtg tct ccc aag acc acg gac ccc gag gag ggc ttt ccc cgc ggg	911
Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly	

210	215	220	
ctg ggg gcc tgc aca ctg ctg ggt tcc ccg cag cac tcc ccc tcc acc			959
Leu Gly Ala Cys Thr Leu Leu Gly Ser Pro Gln His Ser Pro Ser Thr			
225	230	235	240
tgc ccc cgc gcc agc gtc act gag gag agc tgg ctg ggt gcc cgc tcc			1007
Ser Pro Arg Ala Ser Val Thr Glu Glu Ser Trp Leu Gly Ala Arg Ser			
245	250	255	
tcc aga ccc gcg tcc cct tgc aac aag agg aag tac agc ctc aac gcc			1055
Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser Leu Asn Gly			
260	265	270	
cgg cag ccg ccc tac tca ccc cac cac tgc ccc acg ccg tcc ccg cac			1103
Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His			
275	280	285	
ggc tcc ccg cgg gtc agc gtg acc gac gac tgc tgg ttg ggc aac acc			1151
Gly Ser Pro Arg Val Ser Val Thr Asp Asp Ser Trp Leu Gly Asn Thr			
290	295	300	
acc cag tac acc agc tgc gcc atc gtg gcc gcc atc aac gcg ctg acc			1199
Thr Gln Tyr Thr Ser Ser Ala Ile Val Ala Ala Ile Asn Ala Leu Thr			
305	310	315	320
acc gac agc agc ctg gac ctg gga gat ggc gtc cct gtc aag tcc cgc			1247
Thr Asp Ser Ser Leu Asp Leu Gly Asp Gly Val Pro Val Lys Ser Arg			
325	330	335	
aag acc acc ctg gag cag ccg ccc tca gtg gcg ctc aag gtg gag ccc			1295
Lys Thr Thr Leu Glu Gln Pro Pro Ser Val Ala Leu Lys Val Glu Pro			
340	345	350	
gtc ggg gag gac ctg ggc agc ccc ccg ccc ccg gcc gac ttc gcg ccc			1343
Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro			

355	360	365	
gaa gac tac tcc tct ttc cag cac atc agg aag ggc ggc ttc tgc gac			1391
Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp			
370	375	380	
cag tac ctg gcg gtg ccg cag cac ccc tac cag tgg gcg aag ccc aag			1439
Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys			
385	390	395	400
ccc ctg tcc cct acg tcc tac atg agc ccg acc ctg ccc gcc ctg gac			1487
Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp			
405	410	415	
tgg cag ctg ccg tcc cac tca ggc ccg tat gag ctt cgg att gag gtg			1535
Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val			
420	425	430	
cag ccc aag tcc cac cac cga gcc cac tac gag acg gag ggc agc cgg			1583
Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg			
435	440	445	
ggg gcc gtg aag gcg tcc gcc gga gga cac ccc atc gtg cag ctg cat			1631
Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His			
450	455	460	
ggc tac ttg gag aat gag ccg ctg atg ctg cag ctt ttc att ggg acg			1679
Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr			
465	470	475	480
gcg gac gac cgc ctg ctg cgc ccg cac gcc ttc tac cag gtg cac cgc			1727
Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg			
485	490	495	
atc aca ggg aag acc gtg tcc acc acc agc cac gag gct atc ctc tcc			1775

Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser

500

505

510

aac acc aaa gtc ctg gag atc cca ctc ctg ccg gag aac agc atg cga 1823

Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg

515

520

525

gcc gtc att gac tgt gcc gga atc ctg aaa ctc aga aac tcc gac att 1871

Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile

530

535

540

gaa ctt cgg aaa gga gag acg gac atc ggg agg aag aac aca cgg gta 1919

Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val

545

550

555

560

cgg ctg gtg ttc cgc gtt cac gtc ccg caa ccc agc ggc cgc acg ctg 1967

Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu

565

570

575

tcc ctg cag gtg gcc tcc aac ccc atc gaa tgc tcc cag cgc tca gct 2015

Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala

580

585

590

cag gag ctg cct ctg gtg gag aag cag agc acg gac agc tat ccg gtc 2063

Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val

595

600

605

gtg ggc ggg aag aag atg gtc ctg tct ggc cac aac ttc ctg cag gac 2111

Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp

610

615

620

tcc aag gtc att ttc gtg gag aaa gcc cca gat ggc cac cat gtc tgg 2159

Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp

625

630

635

640

gag atg gaa gcg aaa act gac cgg gac ctg tgc aag ccg aat tct ctg 2207

Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu

645

650

655

gtg gtt gag atc ccg cca ttt cgg aat cag agg ata acc agc ccc gtt 2255

Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val

660

665

670

cac gtc agt ttc tac gtc tgc aac ggg aag aga aag cga agc cag tac 2303

His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr

675

680

685

cag cgt ttc acc tac ctt ccc gcc aac ggt aac gcc atc ttt cta acc 2351

Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr

690

695

700

gta agc cgt gaa cat gag cgc gtg ggg tgc ttt ttc taaagacgca 2397

Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe

705

710

715

gaaacgacgt cgccgtaaag cagcgtggcg tgttcacat ttaactgtgt gatgtcccgt 2457

tagtgagacc gagccatcga tgcctgaaa aggaaaggaa aagggaagct tcggatgcat 2517

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ttttgcttct tgcgaatgta taacagccaa ggggaaaaca tggctcttct gtcctcaaaaa 2637

actgaggggg tcttgggtgt catttgcacc ctaaagcigc ttacggtgaa aaggcaaata 2697

ggtatagcta ttttgcaggc accttttagga ataaactttg ctttta 2743

<210> 48

<211> 716

<212> PRT

<213> Homo sapiens

<400> 48

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35	40	45	
Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr			
50	55	60	
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile			
65	70	75	80
Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly			
85	90	95	
Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala			
100	105	110	
Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu			
115	120	125	
Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val			
130	135	140	
Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro			
145	150	155	160
Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser			
165	170	175	
Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn			
180	185	190	
Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro			
195	200	205	
Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly			

210	215	220	
Leu Gly Ala Cys Thr	Leu Leu Gly Ser Pro Gln His	Ser Pro Ser Thr	
225	230	235	240
Ser Pro Arg Ala Ser Val Thr	Glu Glu Ser Trp Leu Gly Ala Arg	Ser	
245	250	255	
Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser Leu Asn Gly			
260	265	270	
Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His			
275	280	285	
Gly Ser Pro Arg Val Ser Val Thr Asp Asp Ser Trp Leu Gly Asn Thr			
290	295	300	
Thr Gln Tyr Thr Ser Ser Ala Ile Val Ala Ala Ile Asn Ala Leu Thr			
305	310	315	320
Thr Asp Ser Ser Leu Asp Leu Gly Asp Gly Val Pro Val Lys Ser Arg			
325	330	335	
Lys Thr Thr Leu Glu Gln Pro Pro Ser Val Ala Leu Lys Val Glu Pro			
340	345	350	
Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro			
355	360	365	
Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp			
370	375	380	
Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys			
385	390	395	400
Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp			
405	410	415	
Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val			
420	425	430	

Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg
 435 440 445
 Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His
 450 455 460
 Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr
 465 470 475 480
 Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg
 485 490 495
 Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser
 500 505 510
 Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg
 515 520 525
 Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile
 530 535 540
 Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val
 545 550 555 560
 Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu
 565 570 575
 Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala
 580 585 590
 Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val
 595 600 605
 Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp
 610 615 620
 Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp
 625 630 635 640

Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu

645

650

655

Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val

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665

670

His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr

675

680

685

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700

Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe

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710

715

<210> 49

<211> 2353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (241).. (1482)

<400> 49

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ccgcccgcct gccgcccctc tccctctgcc ttcctccccc acggccggcc gcctctcgcg 180

ccgcccgcgc gcagccgagg agccgaggcc gccgcccgcg tggcggcgga gccctcagcc 240

atg gcc tcg ggc gac acc ctc tac atc gcc acg gac ggc tcg gag atg 288

Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met

1

5

10

15

ccg gcc gag atc gtg gag ctg cac gag atc gag gtg gag acc atc ccg 336

Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro
20 25 30
gig gag acc atc gag acc aca gtg gtg ggc gag gag gag gag gag gac 384
Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Glu Asp
35 40 45
gac gag gag gag gag ggc ggc ggt ggc gag cac ggc ggc ggg ggc ggc 432
Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly
50 55 60
cac ggg cac gcc ggc cac cac cac cac cat cac cac cac cac cac 480
His Gly His Ala Gly His His His His His His His His His His His
65 70 75 80
ccg ccc atg atc gct ctg cag ccg ctg gtc acc gag gag ccg acc cag 528
Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln
85 90 95
gtg cac cac cac cag gag gtg atc ctg gtg cag acg cgc gag gag gtg 576
Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val
100 105 110
gtg ggc ggc gag gag tgc gag ggg ctg cgc gcc gag gag ggc ttc gag 624
Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu
115 120 125
gat cag att ctc atc ccg gtg ccc gcg ccg gcc ggc ggc gag gag gag 672
Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp
130 135 140
tac att gaa caa acg ctg gtc acc gtg gcg gcg gcc ggc aag agc ggc 720
Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly
145 150 155 160
ggc ggc ggc tgc tgc tgc tgc gga ggc ggc cgc gtc aag aag ggc ggc 768

Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly
 165 170 175
 ggc aag aag agc ggc aag aag agt tac ctc agc ggc ggg gcc ggc gcg 816
 Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala
 180 185 190
 gcg ggc ggg cgc ggc gcc gac ccg ggc aac aag aag tgg gag cag aag 864
 Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys
 195 200 205
 cag gtg cag atc aag acc ctg gag ggc gag ttc tgg gtc acc atg tgg 912
 Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp
 210 215 220
 tcc tca gat gaa aaa aaa gat att gac cat gag aca gtg gtt gaa gaa 960
 Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu
 225 230 235 240
 cag atc att gga gag aac tca cct cct gat tat tca gaa tat atg aca 1008
 Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr
 245 250 255
 gga aag aaa ctt cct cct gga gga ata cct ggc att gac ctc tca gat 1056
 Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp
 260 265 270
 ccc aaa caa ctg gca gaa ttt gct aga atg aag cca aga aaa att aaa 1104
 Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys
 275 280 285
 gaa gat gat gct cca aga aca ata gct tgc cct cat aaa ggc tgc aca 1152
 Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr
 290 295 300

aag atg ttc agg gat aac tgc gcc atg aga aaa cat ctg cac acc cac 1200
Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His
305 310 315 320
ggc ccc aga gtc cac gtc tgt gca gaa tgt ggc aaa gct ttt gtt gag 1248
Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu
325 330 335
agt tca aaa cta aaa cga cac caa ctg gtt cat act gga gag aag ccc 1296
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro
340 345 350
ttt cag tgc acg ttc gaa ggc tgt ggg aaa cgc ttt tca ctg gac ttc 1344
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe
355 360 365
aat ttg cgc aca cat gtg cga atc cat acc gga gac agg ccc tat gtg 1392
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val
370 375 380
tgc ccc ttc gat ggt tgt aat aag aag ttt gct cag tca act aac ctg 1440
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu
385 390 395 400
aaa tct cac atc tta aca cat gct aag gcc aaa aac aac cag 1482
Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
405 410
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 aatactgcca gatgctgatg ttcagtgtaa ttcttttgcc tgttcagtta cagaaagtgg 2262
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 aaagggcaac aataaaatag caatcctaaa g 2353

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<211> 414

<212> PRT

<213> Homo sapiens

<400> 50

Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met

1 5 10 15

Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro

20 25 30

Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Asp

35 40 45

Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly

50 55 60

His Gly His Ala Gly His His His His His His His His His

65 70 75 80

Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln

85 90 95

Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val
 100 105 110
 Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu
 115 120 125
 Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp
 130 135 140
 Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly
 145 150 155 160
 Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly
 165 170 175
 Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala
 180 185 190
 Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys
 195 200 205
 Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp
 210 215 220
 Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu
 225 230 235 240
 Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr
 245 250 255
 Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp
 260 265 270
 Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys
 275 280 285
 Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr
 290 295 300

Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His
 305 310 315 320
 Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu
 325 330 335
 Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro
 340 345 350
 Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe
 355 360 365
 Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val
 370 375 380
 Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu
 385 390 395 400
 Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
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<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222).. (950)

<400> 51

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 ccaacattac ttgagtcitt ggataaaatt gagaaaagag tctacaagta ttgtggactc 180
 tacaggaggc aggaggctga caactggcag taaagacaaa g atg tca ggc ctg cgg 236

Met Ser Gly Leu Arg

1

5

ccc ggc act caa gtg gac cct gag att gag ctt ttt gta aag gct gga 284

Pro Gly Thr Gln Val Asp Pro Glu Ile Glu Leu Phe Val Lys Ala Gly

10

15

20

agt gat gga gag agt att gga aac tgt ccc ttt tgc caa cgc ctt ttc 332

Ser Asp Gly Glu Ser Ile Gly Asn Cys Pro Phe Cys Gln Arg Leu Phe

25

30

35

atg atc ctc tgg ctt aaa gga gtt aaa ttt aat gtg aca act gtt gac 380

Met Ile Leu Trp Leu Lys Gly Val Lys Phe Asn Val Thr Thr Val Asp

40

45

50

atg acc aga aag cct gaa gaa cta aag gac tta gcc cca ggt acc aat 428

Met Thr Arg Lys Pro Glu Glu Leu Lys Asp Leu Ala Pro Gly Thr Asn

55

60

65

cct ccg ttc ctg gtg tat aac aag gag ttg aaa aca gac ttc att aaa 476

Pro Pro Phe Leu Val Tyr Asn Lys Glu Leu Lys Thr Asp Phe Ile Lys

70

75

80

85

att gag gag ttt tta gaa caa acc ctg gct cct cca agg tac cct cac 524

Ile Glu Glu Phe Leu Glu Gln Thr Leu Ala Pro Pro Arg Tyr Pro His

90

95

100

ctg agt ccc aag tac aag gag tct ttt gat gtg ggc tgt aac ctc ttt 572

Leu Ser Pro Lys Tyr Lys Glu Ser Phe Asp Val Gly Cys Asn Leu Phe

105

110

115

gcc aag ttt tct gca tac att aag aat aca caa aag gag gca aat aag 620

Ala Lys Phe Ser Ala Tyr Ile Lys Asn Thr Gln Lys Glu Ala Asn Lys

120

125

130

aat ttt gaa aaa tct ctg ctc aaa gaa ttc aag cgt ctg gat gac tac 668

Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys Arg Leu Asp Asp Tyr
 135 140 145
 tta aac acc cca ctt ctg gat gaa att gat cca gac agt gct ggg gaa 716
 Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro Asp Ser Ala Gly Glu
 150 155 160 165
 ccc cca gtt tcc aga aga cta ttc ttg gat ggg gac cag cta aca ctg 764
 Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly Asp Gln Leu Thr Leu
 170 175 180
 gct gat tgt agc ttg tta ccc aag ctg aac att att aaa gtt gct gcc 812
 Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile Ile Lys Val Ala Ala
 185 190 195
 aag aaa tat cgt gac ttt gac att cca gca gaa ttc tca gga gtc tgg 860
 Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu Phe Ser Gly Val Trp
 200 205 210
 cgt tat ctc cac aat gcc tat gcc cgt gaa gaa ttt acc cac acg tgt 908
 Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu Phe Thr His Thr Cys
 215 220 225
 cct gaa gac aaa gaa att gaa aat act tac gca aat gtg gct 950
 Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala Asn Val Ala
 230 235 240
 taaacagaag agttaggaga gctcttacag gagaaaaggc tatatttgtg atcagatttt 1010
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<211> 243

<212> PRT

<213> Homo sapiens

<400> 52

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Phe Val Lys Ala Gly Ser Asp Gly Glu Ser Ile Gly Asn Cys Pro Phe
20 25 30
Cys Gln Arg Leu Phe Met Ile Leu Trp Leu Lys Gly Val Lys Phe Asn
35 40 45
Val Thr Thr Val Asp Met Thr Arg Lys Pro Glu Glu Leu Lys Asp Leu
50 55 60
Ala Pro Gly Thr Asn Pro Pro Phe Leu Val Tyr Asn Lys Glu Leu Lys
65 70 75 80
Thr Asp Phe Ile Lys Ile Glu Glu Phe Leu Glu Gln Thr Leu Ala Pro
85 90 95
Pro Arg Tyr Pro His Leu Ser Pro Lys Tyr Lys Glu Ser Phe Asp Val
100 105 110
Gly Cys Asn Leu Phe Ala Lys Phe Ser Ala Tyr Ile Lys Asn Thr Gln
115 120 125
Lys Glu Ala Asn Lys Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys
130 135 140
Arg Leu Asp Asp Tyr Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro
145 150 155 160
Asp Ser Ala Gly Glu Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly
165 170 175

Asp Gln Leu Thr Leu Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile

180

185

190

Ile Lys Val Ala Ala Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu

195

200

205

Phe Ser Gly Val Trp Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu

210

215

220

Phe Thr His Thr Cys Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala

225

230

235

240

Asn Val Ala

<210> 53

<211> 4001

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (316)

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Pro Gly Asn Pro Tyr Val Lys Val Asn Val Tyr Tyr Gly Arg Lys Arg

1

5

10

15

att gcc aag aag aaa acc cat gtg aag aag tgc act ttg aac ccc atc 97

Ile Ala Lys Lys Lys Thr His Val Lys Lys Cys Thr Leu Asn Pro Ile

20

25

30

ttc aat gaa tct ttc atc tac gac atc ccc act gac ctc ctg cct gat 145

Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp

35

40

45

atc agc atc gag ttc ctc gtt atc gac ttc gat cgc acc acc aag aat 193
 Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn
 50 55 60
 gag gtg gtg ggg agg ctg atc ctg ggg gca cac agt gtc aca gcc agt 241
 Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser
 65 70 75 80
 ggt gct gaa cac tgg aga gag gtc tgc gag agc ccc cgc aag cct gtg 289
 Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val
 85 90 95
 gcc aag tgg cac agt ctg agc gag tac taatcctgtt cttctctcct 336
 Ala Lys Trp His Ser Leu Ser Glu Tyr
 100 105
 ctaatccccg ggggccaagc tggggagggg tgtggagggg aaaaagatga cagagaagtg 396
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 acatt

4001

<210> 54

<211> 105

<212> PRT

<213> Homo sapiens

<400> 54

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1 5 10 15

Ile Ala Lys Lys Lys Thr His Val Lys Lys Cys Thr Leu Asn Pro Ile

20 25 30

Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp

35 40 45

Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn

50 55 60

Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser

65 70 75 80

Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val

85 90 95

Ala Lys Trp His Ser Leu Ser Glu Tyr

100 105

<210> 55

<211> 952

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118).. (909)

<400> 55

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atg gaa tca ggc ttc acc tcc aag gac acc tat cta agc cat ttt aac 165

Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His Phe Asn

1	5	10	15	
cct cgg gat tac cta gaa aaa tat tac aag ttt ggt tct agg cac tct				213
Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg His Ser				
20	25	30		
gca gaa agc cag att ctt aag cac ctt ctg aaa aat ctt ttc aag ata				261
Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe Lys Ile				
35	40	45		
ttc tgc cta gac ggt gtg aag gga gac ctg ctg att gac atc ggc tct				309
Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile Gly Ser				
50	55	60		
ggc ccc act atc tat cag ctc ctc tct gct tgt gaa tcc ttt aag gag				357
Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu				
65	70	75	80	
atc gtc gtc act gac tac tca gac cag aac ctg cag gag ctg gag aag				405
Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys				
85	90	95		
tgg ctg aag aaa gag cca gag gcc ttt gac tgg tcc cca gtg gtg acc				453
Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr				
100	105	110		
tat gtg tgt gat ctt gaa ggg aac aga gtc aag ggt cca gag aag gag				501
Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu				
115	120	125		
gag aag ttg aga cag gcg gtc aag cag gtg ctg aag tgt gat gtg act				549
Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr				
130	135	140		
cag agc cag cca ctg ggg gcc gtc ccc tta ccc ccg gct gac tgc gtg				597
Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val				

145	150	155	160	
ctc agc aca ctg tgt ctg gat gcc gcc tgc cca gac ctc ccc acc tac				645
Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr				
165	170	175		
tgc agg gcg ctc agg aac ctc ggc agc cta ctg aag cca ggg ggc ttc				693
Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe				
180	185	190		
ctg gtg atc atg gat gcg ctc aag agc agc tac tac atg att ggt gag				741
Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu				
195	200	205		
cag aag ttc tcc agc ctc ccc ctg ggc cgg gag gca gta gag gct gct				789
Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala				
210	215	220		
gtg aaa gag gct ggc tac aca atc gaa tgg ttt gag gtg atc tgc caa				837
Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln				
225	230	235	240	
agt tat tct tcc acc atg gcc aac aac gaa gga ctt ttc tcc ctg gtg				885
Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser Leu Val				
245	250	255		
gcg agg aag ctg agc aga ccc ctg tgatgcctgt gacctcaatt aaagcaattc				939
Ala Arg Lys Leu Ser Arg Pro Leu				
260				
ctttgacctg tca				952

<210> 56

<211> 264

<212> PRT

<213> Homo sapiens

<400> 56

Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His Phe Asn

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Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg His Ser

20 25 30

Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe Lys Ile

35 40 45

Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile Gly Ser

50 55 60

Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe Lys Glu

65 70 75 80

Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys

85 90 95

Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr

100 105 110

Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu Lys Glu

115 120 125

Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr

130 135 140

Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val

145 150 155 160

Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr

165 170 175

Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly Gly Phe

180 185 190

Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile Gly Glu
 195 200 205

Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu Ala Ala
 210 215 220

Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile Ser Gln
 225 230 235 240

Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser Leu Val
 245 250 255

Ala Arg Lys Leu Ser Arg Pro Leu
 260

<210> 57

<211> 2617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (94).. (633)

<400> 57

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Met Ala Pro Gly Val Ala Arg

1

5

ggg ccg acg ccg tac tgg agg ttg cgc ctc ggt ggc gcc gcg ctg ctc 162

Gly Pro Thr Pro Tyr Trp Arg Leu Arg Leu Gly Gly Ala Ala Leu Leu

10

15

20

ctg ctg ctc atc ccg gtg gcc gcc gcg cag gag cct ccc gga gct gct 210

Leu Leu Leu Ile Pro Val Ala Ala Ala Gln Glu Pro Pro Gly Ala Ala
 25 30 35
 tgt tct cag aac aca aac aaa acc tgt gaa gag tgc ctg aag aac gtc 258
 Cys Ser Gln Asn Thr Asn Lys Thr Cys Glu Glu Cys Leu Lys Asn Val
 40 45 50 55
 tcc tgt ctt tgg tgc aac act aac aag gct tgt ctg gac tac cca gtt 306
 Ser Cys Leu Trp Cys Asn Thr Asn Lys Ala Cys Leu Asp Tyr Pro Val
 60 65 70
 aca agc gtc ttg cca ccg gct tcc ctt tgt aaa ttg agc tct gca cgc 354
 Thr Ser Val Leu Pro Pro Ala Ser Leu Cys Lys Leu Ser Ser Ala Arg
 75 80 85
 tgg gga gtt tgt tgg gtg aac ttt gag gcg ctg atc atc acc atg tgc 402
 Trp Gly Val Cys Trp Val Asn Phe Glu Ala Leu Ile Ile Thr Met Ser
 90 95 100
 gla gtc ggg gga acc ctc ctc ctg ggc att gcc atc tgc tgc tgc tgc 450
 Val Val Gly Gly Thr Leu Leu Leu Gly Ile Ala Ile Cys Cys Cys Cys
 105 110 115
 tgc tgc agg agg aag agg agc cgg aag ccg gac agg agt gag gag aag 498
 Cys Cys Arg Arg Lys Arg Ser Arg Lys Pro Asp Arg Ser Glu Glu Lys
 120 125 130 135
 gcc atg cgt gag cgg gag gag agg cgg ata cgg cag gag gaa cgg aga 546
 Ala Met Arg Glu Arg Glu Glu Arg Arg Ile Arg Gln Glu Glu Arg Arg
 140 145 150
 gca gag atg aag aca aga cat gat gaa atc aga aaa aaa tat ggc ctg 594
 Ala Glu Met Lys Thr Arg His Asp Glu Ile Arg Lys Lys Tyr Gly Leu
 155 160 165
 ttt aaa gaa gaa aac ccg tat gct aga ttt gaa aac aac taaagcgtc 643

Phe Lys Glu Glu Asn Pro Tyr Ala Arg Phe Glu Asn Asn

170

175

180

cagcacatca gtcccgacgc ttctgtgag gtgcactccg cagcccagcc cagccgggag 703
 accacgiggc cattgcggic tcttgacctt ggccagtga cctgccagcc ttccaggaca 763
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 gcacccagcg ctgtggctgt cattctccca gggcagaacc ctgcgttict ctctgtccac 1003
 taacaagctt cacacgaac acagggaagt cggtttgact ttgtcatga ggagaactga 1063
 ccagccctca tcatcccca taaaaccag gacagcgtct gtgtgcgcat cttagagtctt 1123
 cacacctgtt gactcacag gcttttgctg atgacacggg gctccaglac acagtcgat 1183
 aaggacttaa cgicctaacc tcaatlgiai taaatagcat iggggaatag cttaaacciti 1243
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 ttgctttggg aaagtaggtc agcagcacct aagatcaagg atgcgttcca ttttcacact 2023
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actgatccag aacacttcaa gaactcgcca aacagctcga taagcccttt tgactgtgta 2143
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 gcttttttct gaaatacact aagagcagcc aaaaaactgt aacctcaagg aaaccataaa 2563
 gcttggagtg ccttaatttt taaccagttt ccaataaaac ggtttactac ctga 2617

<210> 58

<211> 180

<212> PRT

<213> Homo sapiens

<400> 58

Met Ala Pro Gly Val Ala Arg Gly Pro Thr Pro Tyr Trp Arg Leu Arg

1 5 10 15

Leu Gly Gly Ala Ala Leu Leu Leu Leu Ile Pro Val Ala Ala Ala

20 25 30

Gln Glu Pro Pro Gly Ala Ala Cys Ser Gln Asn Thr Asn Lys Thr Cys

35 40 45

Glu Glu Cys Leu Lys Asn Val Ser Cys Leu Trp Cys Asn Thr Asn Lys

50 55 60

Ala Cys Leu Asp Tyr Pro Val Thr Ser Val Leu Pro Pro Ala Ser Leu

65 70 75 80

Cys Lys Leu Ser Ser Ala Arg Trp Gly Val Cys Trp Val Asn Phe Glu

85 90 95

Ala Leu Ile Ile Thr Met Ser Val Val Gly Gly Thr Leu Leu Leu Gly

100

105

110

Ile Ala Ile Cys Cys Cys Cys Cys Cys Arg Arg Lys Arg Ser Arg Lys

115

120

125

Pro Asp Arg Ser Glu Glu Lys Ala Met Arg Glu Arg Glu Glu Arg Arg

130

135

140

Ile Arg Gln Glu Glu Arg Arg Ala Glu Met Lys Thr Arg His Asp Glu

145

150

155

160

Ile Arg Lys Lys Tyr Gly Leu Phe Lys Glu Glu Asn Pro Tyr Ala Arg

165

170

175

Phe Glu Asn Asn

180

<210> 59

<211> 3217

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (469).. (1875)

<400> 59

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 ctccctgttt ccttccctgt ccttcccage tcacgctctc ttccctlgcc gcttgccttt 180
 cttttttcct ttttttgcatt tggcgtcttg gggtgtttac acacacgcgc gctgtccatt 240
 gcagcttaca taaaggcggg cgcgattatg caattatatt gtttagcgata ttccaagagc 300
 aatggctcgt tttcttagga ttccaacacg aaggcatcat gcatttttga aaaactagta 360

ttgagaataa taccttgcaa cgtaaagaat gtttttgggt atttttacac aatctctact 420

ttgaccaaac gagtctggac agttttcttt taatggaaaa taggagaa atg gag gaa 477

Met Glu Glu

1

aga atg gaa atg att tct gaa agg cca aaa gag agt atg tat tcc tgg 525

Arg Met Glu Met Ile Ser Glu Arg Pro Lys Glu Ser Met Tyr Ser Trp

5

10

15

aac aaa act gca gag aaa agt gat ttt gaa gct gta gaa gca ctt atg 573

Asn Lys Thr Ala Glu Lys Ser Asp Phe Glu Ala Val Glu Ala Leu Met

20

25

30

35

tca atg agc tgc agt tgg aag tct gat ttt aag aaa tac gtt gaa aac 621

Ser Met Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr Val Glu Asn

40

45

50

aga cct gtt aca cca gta tct gat ttg tca gag gaa gag aat ctg ctt 669

Arg Pro Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu Asn Leu Leu

55

60

65

ccg gga aca cct gat ttt cat aca atc cca gca ttt tgt ttg act cca 717

Pro Gly Thr Pro Asp Phe His Thr Ile Pro Ala Phe Cys Leu Thr Pro

70

75

80

cct lac agt cct tct gac ttt gaa ccc tct caa gtg tca aat ctg atg 765

Pro Tyr Ser Pro Ser Asp Phe Glu Pro Ser Gln Val Ser Asn Leu Met

85

90

95

gca cca gcg cca tct act gta cac ttc aag tca ctc tca gat act gcc 813

Ala Pro Ala Pro Ser Thr Val His Phe Lys Ser Leu Ser Asp Thr Ala

100

105

110

115

aaa cct cac att gcc gca cct ttc aaa gag gaa gaa aag agc cca gta 861

Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Glu Lys Ser Pro Val

120	125	130	
tct gcc ccc aaa ctc ccc aaa gct cag gca aca agt gtg att cgt cat			909
Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His			
135	140	145	
aca gct gat gcc cag cta tgt aac cac cag acc tgc cca atg aaa gca			957
Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro Met Lys Ala			
150	155	160	
gcc agc atc ctc aac tat cag aac aat tct ttt aga aga aga acc cac			1005
Ala Ser Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg Arg Thr His			
165	170	175	
cta aat gtt gag gct gca aga aag aac ata cca tgt gcc gct gtg tca			1053
Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala Ala Val Ser			
180	185	190	195
cca aac aga tcc aaa tgt gag aga aac aca gtg gca gat gtt gat gag			1101
Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp Val Asp Glu			
200	205	210	
aaa gca agt gct gca ctt tat gac ttt tct gtg cct tcc tca gag acg			1149
Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser Ser Glu Thr			
215	220	225	
gtc atc tgc agg tct cag cca gcc cct gtg tcc cca caa cag aag tca			1197
Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln Gln Lys Ser			
230	235	240	
gtg ttg gtc tct cca cct gca gta tct gca ggg gga gtg cca cct atg			1245
Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val Pro Pro Met			
245	250	255	
ccg gtc atc tgc cag atg gtt ccc ctt cct gcc aac aac cct gtt gtg			1293

Pro Val Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn Pro Val Val
 260 265 270 275
 aca aca gtc gtt ccc agc act cct ccc agc cag cca cca gct gtt tgc 1341
 Thr Thr Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro Ala Val Cys
 280 285 290
 ccc cct gtt gtg ttc atg ggc aca caa gtc ccc aaa ggc gct gtc atg 1389
 Pro Pro Val Val Phe Met Gly Thr Gln Val Pro Lys Gly Ala Val Met
 295 300 305
 ttt gtg gta ccc cag ccc gtt gtg cag agt tca aag cct ccg gtg gtg 1437
 Phe Val Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro Pro Val Val
 310 315 320
 agc ccg aat ggc acc aga ctc tct ccc att gcc cct gct cct ggg ttt 1485
 Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe
 325 330 335
 tcc cct tca gca gca aaa gtc act cct cag att gat tca tca agg ata 1533
 Ser Pro Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser Ser Arg Ile
 340 345 350 355
 agg agt cac atc tgt agc cac cca gga tgt ggc aag aca tac ttt aaa 1581
 Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr Tyr Phe Lys
 360 365 370
 agt tcc cat ctg aag gcc cac acg agg acg cac aca gga gaa aag cct 1629
 Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly Glu Lys Pro
 375 380 385
 ttc agc tgt agc tgg aaa ggt tgt gaa agg agg ttt gcc cgt tct gat 1677
 Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp
 390 395 400
 gaa ctg tcc aga cac agg cga acc cac acg ggl gag aag aaa ttt gcg 1725

Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala
 405 410 415
 tgc ccc atg tgt gac cgg cgg ttc atg agg agt gac cat ttg acc aag 1773
 Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys
 420 425 430 435
 cat gcc cgg cgc cat cta tca gcc aag aag cta cca aac tgg cag atg 1821
 His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met
 440 445 450
 gaa gtg agc aag cta aat gac att gct cta cct cca acc cct gct ccc 1869
 Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr Pro Ala Pro
 455 460 465
 aca cag tgacagaccg gaaagtgaag agtcagaact aactttggtc tcagcgggag 1925
 Thr Gln
 ccagtggtga tgtaaaaatg cttccactgc aagtctgtgg cccacaacg tggcttaaag 1985
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gaagatgaaa tatatatigt aaagaaggga tattaagaat cttagataac ttcttgaaaa 2765
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 tgaattagaa aattagtgac cattattcac aggtggacaa atgttgctct gttaatltat 2885
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 aagtacattg cttaaaatat atagtgtaaa atgtcactat atcttcccat ttaacattgt 3065
 ttttgtatat tgggtgtaga ttcttgacat caaaacttgg acccttggaa aacaaaagtt 3125
 ttaattaaaa aaaatccttg tgacttaciaa ttgcacaat atttcttttg ttgtacttta 3185
 tatcttgttt acaataaaga attccctttg gc 3217

<210> 60

<211> 469

<212> PRT

<213> Homo sapiens

<400> 60

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Tyr	Ser	Trp	Asn	Lys	Thr	Ala	Glu	Lys	Ser	Asp	Phe	Glu	Ala	Val	Glu
				20				25					30		
Ala	Leu	Met	Ser	Met	Ser	Cys	Ser	Trp	Lys	Ser	Asp	Phe	Lys	Lys	Tyr
				35				40					45		
Val	Glu	Asn	Arg	Pro	Val	Thr	Pro	Val	Ser	Asp	Leu	Ser	Glu	Glu	Glu
				50				55					60		
Asn	Leu	Leu	Pro	Gly	Thr	Pro	Asp	Phe	His	Thr	Ile	Pro	Ala	Phe	Cys
				65				70					75		80
Leu	Thr	Pro	Pro	Tyr	Ser	Pro	Ser	Asp	Phe	Glu	Pro	Ser	Gln	Val	Ser
								85					90		95

Asn Leu Met Ala Pro Ala Pro Ser Thr Val His Phe Lys Ser Leu Ser
100 105 110
Asp Thr Ala Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Glu Lys
115 120 125
Ser Pro Val Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val
130 135 140
Ile Arg His Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro
145 150 155 160
Met Lys Ala Ala Ser Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg
165 170 175
Arg Thr His Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala
180 185 190
Ala Val Ser Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp
195 200 205
Val Asp Glu Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser
210 215 220
Ser Glu Thr Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln
225 230 235 240
Gln Lys Ser Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val
245 250 255
Pro Pro Met Pro Val Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn
260 265 270
Pro Val Val Thr Thr Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro
275 280 285
Ala Val Cys Pro Pro Val Val Phe Met Gly Thr Gln Val Pro Lys Gly
290 295 300
Ala Val Met Phe Val Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro

305 310 315 320
 Pro Val Val Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala
 325 330 335
 Pro Gly Phe Ser Pro Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser
 340 345 350
 Ser Arg Ile Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr
 355 360 365
 Tyr Phe Lys Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly
 370 375 380
 Glu Lys Pro Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala
 385 390 395 400
 Arg Ser Asp Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys
 405 410 415
 Lys Phe Ala Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His
 420 425 430
 Leu Thr Lys His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn
 435 440 445
 Trp Gln Met Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr
 450 455 460
 Pro Ala Pro Thr Gln
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<210> 61

<211> 1428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125).. (868)

<400> 61

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 cgcc atg tgc gga ggt ggt gtg att cgt ggc ccc gca ggg aac aac gat 169

Met Ser Gly Gly Gly Val Ile Arg Gly Pro Ala Gly Asn Asn Asp

1 5 10 15

tgc cgc atc tac gtg ggt aac tta cct cca gac atc cga acc aag gac 217

Cys Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp

20 25 30

att gag gac gtg ttc tac aaa tac ggc gct atc cgc gac atc gac ctc 265

Ile Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu

35 40 45

aag aat cgc cgc ggg gga ccg ccc ttc gcc ttc gtt gag ttc gag gac 313

Lys Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp

50 55 60

ccg cga gac gcg gaa gac gcg gtg tat ggt cgc gac ggc tat gat tac 361

Pro Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr

65 70 75

gat ggg lac cgt ctg cgg gtg gag ttt cct cga agc ggc cgt gga aca 409

Asp Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr

80 85 90 95

ggc cga ggc ggc ggc ggg ggt gga ggt ggc gga gct ccc cga ggt cgc 457

Gly Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg

100 105 110

tat ggc ccc cca tcc agg cgg tct gaa aac aga gtg gtt gtc tct gga	505
Tyr Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly	
115 120 125	
ctg cct cca agt gga agt tgg cag gat tta aag gat cac atg cgt gaa	553
Leu Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu	
130 135 140	
gca ggt gat gta tgt tat gct gat gtt tac cga gat ggc act ggt gtc	601
Ala Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val	
145 150 155	
gtg gag ttt gta cgg aaa gaa gat atg acc tat gca gtt cga aaa ctg	649
Val Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu	
160 165 170 175	
gat aac act aag ttt aga tct cat gag gga gaa act gcc tac atc cgg	697
Asp Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg	
180 185 190	
gtt aaa gtt gat ggg ccc aga agt cca agt tat gga aga tct cga tct	745
Val Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser	
195 200 205	
cga agc cgt agt cgt agc aga agc cgt agc aga agc aac agc agg agt	793
Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser	
210 215 220	
cgc agt tac tcc cca agg aga agc aga gga tca cca cgc tat tct ccc	841
Arg Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro	
225 230 235	
cgt cat agc aga tct cgc tct cgt aca taagatgatt ggtgacactt	888
Arg His Ser Arg Ser Arg Ser Arg Thr	
240 245	

ttgtagaac ccatgttgta tacaglttcc ctttattcag tacaatcttt tcatttttta 948
 attcaaactg ttttgttcag aatgggctaa agtgttgaat tgcattcttg taatatcccc 1008
 ttgctcctaa catctacatt cccctcgtgt ctttgataaa ttgtatttta agtgaigtca 1068
 tagacaggat tgttttaaatt tagttaactc calactcttc agactgtgat attgtgtaaa 1128
 tgtctatctg cccctggttg tgtgaactgg gatgttgggg gtgtttgtgg ttatcttacc 1188
 tggggaagtt ctttaigtta tcttgccttt catgtgtctt tctgtagaca taltgaaga 1248
 gatggattaa gaatgccttg gattaaggat tgtggagcac attcaatca ttttaggatt 1308
 gtcaaaagga ggattgagga ggaacagatc aataatggag gcaatggtat gactccaagt 1368
 gctattgtca cagatgaaat tggcagtatt gaccttatac taaaaggcag gggctaaaaa 1428

<210> 62

<211> 248

<212> PRT

<213> Homo sapiens

<400> 62

Met Ser Gly Gly Gly Val Ile Arg Gly Pro Ala Gly Asn Asn Asp Cys

1 5 10 15

Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp Ile

20 25 30

Glu Asp Val Phe Tyr Lys Tyr Gly Ala Ile Arg Asp Ile Asp Leu Lys

35 40 45

Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp Pro

50 55 60

Arg Asp Ala Glu Asp Ala Val Tyr Gly Arg Asp Gly Tyr Asp Tyr Asp

65 70 75 80

Gly Tyr Arg Leu Arg Val Glu Phe Pro Arg Ser Gly Arg Gly Thr Gly

85 90 95

Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Arg Gly Arg Tyr
 100 105 110
 Gly Pro Pro Ser Arg Arg Ser Glu Asn Arg Val Val Val Ser Gly Leu
 115 120 125
 Pro Pro Ser Gly Ser Trp Gln Asp Leu Lys Asp His Met Arg Glu Ala
 130 135 140
 Gly Asp Val Cys Tyr Ala Asp Val Tyr Arg Asp Gly Thr Gly Val Val
 145 150 155 160
 Glu Phe Val Arg Lys Glu Asp Met Thr Tyr Ala Val Arg Lys Leu Asp
 165 170 175
 Asn Thr Lys Phe Arg Ser His Glu Gly Glu Thr Ala Tyr Ile Arg Val
 180 185 190
 Lys Val Asp Gly Pro Arg Ser Pro Ser Tyr Gly Arg Ser Arg Ser Arg
 195 200 205
 Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Asn Ser Arg Ser Arg
 210 215 220
 Ser Tyr Ser Pro Arg Arg Ser Arg Gly Ser Pro Arg Tyr Ser Pro Arg
 225 230 235 240
 His Ser Arg Ser Arg Ser Arg Thr
 245

<210> 63

<211> 3664

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (195).. (1943)

<400> 63

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 ccccaggact tctgtgactc ctgggccaca gaggccaac cagggttaagg gcctggggat 120
 accccctgcc tggccccctt gcccaactg gcaggggggc caggctgggc agcagccct 180
 ctttcacctc aact atg gat ctc ctg ccc ccc aag ccc aag tac aat cca 230

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro

1 5 10

ctc cgg aat gag tct ctg tca tcg ctg gag gaa ggg gct tct ggg tcc 278

Leu Arg Asn Glu Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser

15 20 25

acc ccc ccg gag gag ctg cct tcc cca tca gct tca tcc ctg ggg ccc 326

Thr Pro Pro Glu Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro

30 35 40

atc ctg cct cct ctg cct ggg gac gat agt ccc act acc ctg tgc tcc 374

Ile Leu Pro Pro Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser

45 50 55 60

ttc ttc ccc cgg atg agc aac ctg agg ctg gcc aac ccg gct ggg ggg 422

Phe Phe Pro Arg Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly

65 70 75

cgc cca ggg tct aag ggg gag cca gga agg gca gct gat gat ggg gag 470

Arg Pro Gly Ser Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu

80 85 90

ggg atc gat ggg gca gcc atg cca gag tca ggc ccc cta ccc ctc ctc 518

Gly Ile Asp Gly Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu

95 100 105

cag gac atg aac aag ctg agt gga ggc ggc ggg cgc agg act cgg gtg 566
 Gln Asp Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val
 110 115 120
 gaa ggg ggc cag ctt ggg ggc gag gag tgg acc cgc cac ggg agc ttt 614
 Glu Gly Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe
 125 130 135 140
 gtc aat aag ccc acg cgg ggc tgg ctg cat ccc aac gac aaa gtc atg 662
 Val Asn Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met
 145 150 155
 gga ccc ggg gtt tcc tac ttg gtt cgg tac atg ggt tgt gtg gag gtc 710
 Gly Pro Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val
 160 165 170
 ctc cag tca atg cgt gcc ctg gac ttc aac acc cgg act cag gtc acc 758
 Leu Gln Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr
 175 180 185
 agg gag gcc atc agt ctg gtg tgt gag gct gtg ccg ggt gct aag ggg 806
 Arg Glu Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly
 190 195 200
 gcg aca agg agg aga aag ccc tgt agc cgc ccg ctc agc tct atc ctg 854
 Ala Thr Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu
 205 210 215 220
 ggg agg agt aac ctg aaa ttt gct gga atg cca atc act ctc acc gtc 902
 Gly Arg Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val
 225 230 235
 tcc acc agc agc ctc aac ctc atg gcc gca gac tgc aaa cag atc atc 950
 Ser Thr Ser Ser Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile
 240 245 250

gcc aac cac cac atg caa tct atc tca ttt gca tcc ggc ggg gat ccg 998
 Ala Asn His His Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro
 255 260 265
 gac aca gcc gag tat glc gcc tat gtt gcc aaa gac cct gtg aat cag 1046
 Asp Thr Ala Glu Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln
 270 275 280
 aga gcc tgc cac att ctg gag tgt ccc gaa ggg ctt gcc cag gat gtc 1094
 Arg Ala Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val
 285 290 295 300
 atc agc acc att ggc cag gcc ttc gag ttg cgc ttc aaa caa tac ctc 1142
 Ile Ser Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu
 305 310 315
 agg aac cca ccc aaa ctg glc acc cct cat gac agg atg gct ggc ttt 1190
 Arg Asn Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe
 320 325 330
 gat ggc tca gca tgg gat gag gag gag gaa gag cca cct gac cat cag 1238
 Asp Gly Ser Ala Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln
 335 340 345
 tac tat aat gac ttc ccg ggg aag gaa ccc ccc ttg ggg ggg gtg gta 1286
 Tyr Tyr Asn Asp Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val
 350 355 360
 gac atg agg ctt cgg gaa gga gcc gct cca ggg gct gct cga ccc act 1334
 Asp Met Arg Leu Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr
 365 370 375 380
 gca ccc aat gcc cag acc ccc agc cac ttg gga gct aca ttg cct gta 1382
 Ala Pro Asn Ala Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val

385	390	395	
gga cag cct gtt ggg gga gat cca gaa gtc cgc aaa cag atg cca cct			1430
Gly Gln Pro Val Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro			
400	405	410	
cca cca ccc tgt cca ggc aga gag ctt ttt gat gat ccc tcc tat gtc			1478
Pro Pro Pro Cys Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val			
415	420	425	
aac gtc cag aac cta gac aag gcc cgg caa gca gtg ggt ggt gct ggg			1526
Asn Val Gln Asn Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly			
430	435	440	
ccc ccc aat cct gct atc aat ggc agt gca ccc cgg gac ctg ttt gac			1574
Pro Pro Asn Pro Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp			
445	450	455	460
atg aag ccc ttc gaa gat gct ctt cgg gtg cct cca cct ccc cag tcg			1622
Met Lys Pro Phe Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser			
465	470	475	
gtg tcc atg gct gag cag ctc cga ggg gag ccc tgg ttc cat ggg aag			1670
Val Ser Met Ala Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys			
480	485	490	
ctg agc cgg cgg gag gct gag gca ctg ctg cag ctc aat ggg gac ttc			1718
Leu Ser Arg Arg Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe			
495	500	505	
ttg gta cgg gag agc acg acc aca cct ggc cag tat gtg ctc act ggc			1766
Leu Val Arg Glu Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly			
510	515	520	
ttg cag agt ggg cag cct aag cat ttg cta ctg gtg gac cct gag ggt			1814
Leu Gln Ser Gly Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly			

525 530 535 540
 gtg gtt cgg act aag gat cac cgc ttt gaa agt gtc agt cac ctt atc 1862
 Val Val Arg Thr Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile
 545 550 555
 agc tac cac atg gac aat cac ttg ccc atc atc tct gcg ggc agc gaa 1910
 Ser Tyr His Met Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu
 560 565 570
 ctg tgt cta cag caa cct gtg gag cgg aaa ctg tgatctgccc tagcgtcttc 1963
 Leu Cys Leu Gln Gln Pro Val Glu Arg Lys Leu
 575 580
 ttccagaaga tgcctccaa tccctccac cctatccct aactctcggg acctcgtttg 2023
 ggagigtict gtggccttgg ccttgiglea gagctgggag tagcatggac tctgggttgc 2083
 atatecagct gaglgagagg gtttgagta aaagcctggg tgagaatcct gcctctcccc 2143
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 atgcaacct tagagattgc ccagagccc cactccggc caggcgggag atggacctt 2623
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 ggctcttgt acagttaact ctcccaggtg gattttgtg aggtgagaaa aggggcattg 2863
 agactataaa gcagtagaca atccccacat accatctgta gatttggaa tgcattcttt 2923

taaagtttta tatgcalata ttttagggct gctagactta ctctectatt ttcttttcca 2983
 ttgcttatic ttgagcacia aatgalaalc aattattaca ttataacalc acctttttga 3043
 ctlttccaag cccltttaca gctcttggca ttttctctgc ctaggccctgt gaggtiaactg 3103
 ggatcgcacc ttttatacca gagacctgag gcagatgaaa ttatattcca tctaggacta 3163
 gaaaaacttg ggtctcttac cgcgagactg agaggcagaa gtcagcccga atgacctgtca 3223
 gtttcatgga ggggaaacgc aaaacctgca gtacctgagt accttctaca ggccccggccc 3283
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 aaaaaaaaaa tacatttata catcaccttt ttgacttttc caagcccttt tacagctctt 3523
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 actgagaggc agaagtcagc c 3664

<210> 64

<211> 583

<212> PRT

<213> Homo sapiens

<400> 64

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro Leu Arg Asn Glu

1 5 10 15

Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser Thr Pro Pro Glu

20 25 30

Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro

35 40 45

Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg

50 55 60

Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly Arg Pro Gly Ser
 65 70 75 80
 Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu Gly Ile Asp Gly
 85 90 95
 Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu Gln Asp Met Asn
 100 105 110
 Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly Gly Gln
 115 120 125
 Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn Lys Pro
 130 135 140
 Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro Gly Val
 145 150 155 160
 Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln Ser Met
 165 170 175
 Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu Ala Ile
 180 185 190
 Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr Arg Arg
 195 200 205
 Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg Ser Asn
 210 215 220
 Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr Ser Ser
 225 230 235 240
 Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn His His
 245 250 255
 Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr Ala Glu
 260 265 270
 Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala Cys His

275	280	285	
Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser Thr Ile			
290	295	300	
Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn Pro Pro			
305	310	315	320
Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly Ser Ala			
325	330	335	
Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr Asn Asp			
340	345	350	
Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met Arg Leu			
355	360	365	
Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro Asn Ala			
370	375	380	
Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln Pro Val			
385	390	395	400
Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro Pro Cys			
405	410	415	
Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val Gln Asn			
420	425	430	
Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro Asn Pro			
435	440	445	
Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe			
450	455	460	
Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser Met Ala			
465	470	475	480
Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg			

485	490	495	
Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu			
500	505	510	
Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly			
515	520	525	
Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr			
530	535	540	
Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met			
545	550	555	560
Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln			
565	570	575	
Gln Pro Val Glu Arg Lys Leu			
580			

<210> 65

<211> 2493

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (41).. (1237)

<400> 65

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Met Lys Met Arg Phe

1

5

ttg ggg ttg gtg gtc tgt ttg gtt ctc tgg ccc ctg cat tct gag ggg 103

Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro Leu His Ser Glu Gly

10	15	20	
tct gga ggg aaa ctg aca gct gtg gat cct gaa aca aac atg aat gtg			151
Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu Thr Asn Met Asn Val			
25	30	35	
agt gaa att atc tct tac tgg gga ttc cct agt gag gaa tac cta gtt			199
Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser Glu Glu Tyr Leu Val			
40	45	50	
gag aca gaa gat gga tat att ctg tgc ctt aac cga att cct cat ggg			247
Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn Arg Ile Pro His Gly			
55	60	65	
agg aag aac cat tct gac aaa ggt ccc aaa cca gtt gtc ttc ctg caa			295
Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro Val Val Phe Leu Gln			
70	75	80	85
cat ggc ttg ctg gca gat tct agt aac tgg gtc aca aac ctt gcc aac			343
His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val Thr Asn Leu Ala Asn			
90	95	100	
agc agc ctg ggc ttc att ctt gct gat gct ggt ttt gac gtg tgg atg			391
Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly Phe Asp Val Trp Met			
105	110	115	
ggc aac agc aga gga aat acc tgg tct cgg aaa cat aag aca ctc tca			439
Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Lys Thr Leu Ser			
120	125	130	
glt tct cag gat gaa ttc tgg gct ttc agt tat gat gag atg gca aaa			487
Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu Met Ala Lys			
135	140	145	
tat gac cta cca gct tcc att aac ttc att ctg aat aaa act ggc caa			535
Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu Asn Lys Thr Gly Gln			

150	155	160	165	
gaa caa gtg tat tat gtg ggt cat tct caa ggc acc act ala ggt ttt				583
Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly Thr Thr Ile Gly Phe				
	170	175	180	
ata gca ttt tca cag atc cct gag ctg gct aaa agg att aaa atg ttt				631
Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys Arg Ile Lys Met Phe				
	185	190	195	
ttt gcc ctg ggt cct gtg gct tcc gtc gcc ttc tgt act agc cct atg				679
Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe Cys Thr Ser Pro Met				
	200	205	210	
gcc aaa tta gga cga tta cca gat cat ctc att aag gac tta ttt gga				727
Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile Lys Asp Leu Phe Gly				
	215	220	225	
gac aaa gaa ttt ctt ccc cag agt gcg ttt ttg aag tgg ctg ggt acc				775
Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu Lys Trp Leu Gly Thr				
230	235	240	245	
cac gtt tgc act cat gtc ata ctg aag gag ctc tgt gga aat ctc tgt				823
His Val Cys Thr His Val Ile Leu Lys Glu Leu Cys Gly Asn Leu Cys				
	250	255	260	
ttt ctt ctg tgt gga ttt aat gag aga aat tta aat atg tct aga gtg				871
Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu Asn Met Ser Arg Val				
	265	270	275	
gat gta tat aca aca cat tct cct gct gga act tct gtg caa aac atg				919
Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr Ser Val Gln Asn Met				
	280	285	290	
tta cac tgg agc cag gct gtt aaa ttc caa aag ttt caa gcc ttt gac				967

Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys Phe Gln Ala Phe Asp
 295 300 305
 tgg gga agc agt gcc aag aat tat ttt cat tac aac cag agt tat cct 1015
 Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr Asn Gln Ser Tyr Pro
 310 315 320 325
 ccc aca tac aat gtg aag gac atg ctt gtg ccg act gca gtc tgg agc 1063
 Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro Thr Ala Val Trp Ser
 330 335 340
 ggg ggt cac gac tgg ctt gca gat gtc tac gac gtc aat atc tta ctg 1111
 Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp Val Asn Ile Leu Leu
 345 350 355
 act cag atc acc aac ttg gtg ttc cat gag agc att ccg gaa tgg gag 1159
 Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser Ile Pro Glu Trp Glu
 360 365 370
 cat ctt gac ttc att tgg ggc ctg gat gcc cct tgg agg ctt tat aat 1207
 His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro Trp Arg Leu Tyr Asn
 375 380 385
 aaa att att aat cta atg agg aaa tat cag tgaaagctgg acttgagctg 1257
 Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln
 390 395
 tgiaccacca agtcaatgat tatgtcatgt gaaaatgtgt ttgcttcatt tctgtaaaac 1317
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 gggaagtcga tatttgcctg cttttcttgc agcatcatit ccttacaata ctgtccgggtg 2337
 gacaaaaiga caatigatai gttttcttga tataattact ttagctgcac taacagtaca 2397
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 aacttttcaa taaaattgag tgagacttat aggcc 2493

<210> 66

<211> 399

<212> PRT

<213> Homo sapiens

<400> 66

Met Lys Met Arg Phe Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro

1

5

10

15

Leu His Ser Glu Gly Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu

20

25

30

Thr Asn Met Asn Val Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser

35

40

45

Glu Glu Tyr Leu Val Glu Thr Glu Asp Gly Tyr Ile Leu Cys Leu Asn

50	55	60	
Arg Ile Pro His Gly Arg Lys Asn His Ser Asp Lys Gly Pro Lys Pro			
65	70	75	80
Val Val Phe Leu Gln His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val			
	85	90	95
Thr Asn Leu Ala Asn Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly			
100	105	110	
Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys			
115	120	125	
His Lys Thr Leu Ser Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr			
130	135	140	
Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu			
145	150	155	160
Asn Lys Thr Gly Gln Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly			
	165	170	175
Thr Thr Ile Gly Phe Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys			
180	185	190	
Arg Ile Lys Met Phe Phe Ala Leu Gly Pro Val Ala Ser Val Ala Phe			
195	200	205	
Cys Thr Ser Pro Met Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile			
210	215	220	
Lys Asp Leu Phe Gly Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu			
225	230	235	240
Lys Trp Leu Gly Thr His Val Cys Thr His Val Ile Leu Lys Glu Leu			
	245	250	255
Cys Gly Asn Leu Cys Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu			

260	265	270	
Asn Met Ser Arg Val Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr			
275	280	285	
Ser Val Gln Asn Met Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys			
290	295	300	
Phe Gln Ala Phe Asp Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr			
305	310	315	320
Asn Gln Ser Tyr Pro Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro			
325	330	335	
Thr Ala Val Trp Ser Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp			
340	345	350	
Val Asn Ile Leu Leu Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser			
355	360	365	
Ile Pro Glu Trp Glu His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro			
370	375	380	
Trp Arg Leu Tyr Asn Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln			
385	390	395	

<210> 67

<211> 1633

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (323).. (1177)

<400> 67

aacttaatgt ttttgcattg gactttgagt taagattatt ttttaaacc ttaggactag 60

cattaattga cagctgaccc aggtgctaca cagaagtigga ttcagtgaat ctaggaagac 120
 agcagcagac aggatccag gaaccagtgt ttgatgaagc taggactgag gagcaagcga 180
 gcaagcagca gticgtggaa tctgtctgc tgcgtcttc ctggtttagg agccgacggg 240
 cgctcgcagg ctccagcgcg gctgcccgcg gcaggaccgc gccgcctccg ccgcccgcgc 300
 cgccccctaa cctcccgaag cc atg gcc ggg ctc ggc cac ccc gcc gcc ttc 352

Met Ala Gly Leu Gly His Pro Ala Ala Phe

1 5 10

ggc cgg gcc acc cac gcc gtg gtg cgg gcg cta ccc gag tcg ctc ggc 400
 Gly Arg Ala Thr His Ala Val Val Arg Ala Leu Pro Glu Ser Leu Gly

15 20 25

cag cac gcg ctg aga agc gcc aag ggc gag gag gtg gac gtc gcc cgc 448
 Gln His Ala Leu Arg Ser Ala Lys Gly Glu Glu Val Asp Val Ala Arg

30 35 40

gcg gaa cgg cag cac cag ctc tac gtg ggc gtg ctg ggc agc aag ctg 496
 Ala Glu Arg Gln His Gln Leu Tyr Val Gly Val Leu Gly Ser Lys Leu

45 50 55

ggg ctg cag gtg gtg gag ctg ccg gcc gac gag agc ctt ccg gac tgc 544
 Gly Leu Gln Val Val Glu Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys

60 65 70

gtc ttc gtg gag gac gtg gcc gtg gtg tgc gag gag acg gcc ctc atc 592
 Val Phe Val Glu Asp Val Ala Val Val Cys Glu Glu Thr Ala Leu Ile

75 80 85 90

acc cga ccc ggg gcg ccg agc cgg agg aag gag gtt gac atg atg aaa 640
 Thr Arg Pro Gly Ala Pro Ser Arg Arg Lys Glu Val Asp Met Met Lys

95 100 105

gaa gca tta gaa aaa ctt cag ctc aat ata gta gag atg aaa gat gaa 688
 Glu Ala Leu Glu Lys Leu Gln Leu Asn Ile Val Glu Met Lys Asp Glu

110	115	120	
aat gca act tta gat ggc gga gat gtt tta ttc aca ggc aga gaa ttt			736
Asn Ala Thr Leu Asp Gly Gly Asp Val Leu Phe Thr Gly Arg Glu Phe			
125	130	135	
ttt gtg ggc ctt tcc aaa agg aca aat caa cga ggt gct gaa atc ttg			784
Phe Val Gly Leu Ser Lys Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu			
140	145	150	
gct gat act ttt aag gac tat gca gtc tcc aca gtg cca gtg gca gat			832
Ala Asp Thr Phe Lys Asp Tyr Ala Val Ser Thr Val Pro Val Ala Asp			
155	160	165	170
ggg ttg cat ttg aag agt ttc tgc agc atg gct ggg cct aac ctg atc			880
Gly Leu His Leu Lys Ser Phe Cys Ser Met Ala Gly Pro Asn Leu Ile			
175	180	185	
gca att ggg tct agt gaa tct gca cag aag gcc ctt aag atc atg caa			928
Ala Ile Gly Ser Ser Glu Ser Ala Gln Lys Ala Leu Lys Ile Met Gln			
190	195	200	
cag atg agt gac cac cgc tac gac aaa ctc act gtg cct gat gac ata			976
Gln Met Ser Asp His Arg Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile			
205	210	215	
gca gca aac tgt ata tat cta aat atc ccc aac aaa ggg cac gtc ttg			1024
Ala Ala Asn Cys Ile Tyr Leu Asn Ile Pro Asn Lys Gly His Val Leu			
220	225	230	
ctg cac cga acc ccg gaa gag tat cca gaa agt gca aag gtt tat gag			1072
Leu His Arg Thr Pro Glu Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu			
235	240	245	250
aaa ctg aag gac cat atg ctg atc ccc gtg agc atg tct gaa ctg gaa			1120

Lys Leu Lys Asp His Met Leu Ile Pro Val Ser Met Ser Glu Leu Glu

255

260

265

aag gtg gat ggg ctg ctc acc tgc tgc tca gtt tta att aac aag aaa 1168

Lys Val Asp Gly Leu Leu Thr Cys Cys Ser Val Leu Ile Asn Lys Lys

270

275

280

gta gac tcc tgagctgcag agtccccccc ggtagccggc aagaccgcac 1217

Val Asp Ser

285

aggcaaggcc gatgactctg tgcccactcc tgttgtttcc ctgacaatc tactgtgcca 1277

ctgtgtact aactcttgtt tacaaaattt gattctaagl tgaattgctt cattcaacac 1337

ccccaccctc cctccccrcg aggtggtacc taagctgtgg atttgctaaa tgaattaagc 1397

aacctagaag atacagagct aatgaattat caaaatgta ttaatcccag taaggaaaca 1457

ctcatctagt gtctgtatct ttggtgtnaa aattatctag ttgccagtat attctgaaga 1517

atgtctctct gtcagctcag ataagcttgc tttttttttt ttttttcat gaatcatgtt 1577

tggctccigt gaaagtcctt ggtccaggga tctctctctt ttctcttita cttctg 1633

<210> 68

<211> 285

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Gly Leu Gly His Pro Ala Ala Phe Gly Arg Ala Thr His Ala

1

5

10

15

Val Val Arg Ala Leu Pro Glu Ser Leu Gly Gln His Ala Leu Arg Ser

20

25

30

Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln

35

40

45

Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu
 50 55 60
 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
 65 70 75 80
 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
 85 90 95
 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
 100 105 110
 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
 115 120 125
 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
 130 135 140
 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
 145 150 155 160
 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
 165 170 175
 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
 180 185 190
 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
 195 200 205
 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
 210 215 220
 Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
 225 230 235 240
 Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
 245 250 255
 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu

260 265 270
 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser

275 280 285

<210> 69

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147).. (1421)

<400> 69

aagcgccgtg ctgaacctct gccagtcctg gagactggig cctgagctc caaccagcgg 60
 gcctcatcta caccctcacc accgcaactt ctaccccgag caagaagcag ctcccagaga 120
 gaaagaacgt tcccacctgc ctagcc atg gga gag gac gct gca cag gcc gaa 173

Met Gly Glu Asp Ala Ala Gln Ala Glu

1 5

aag ttc cag cac cct ggg tct gac atg cgg cag gaa aag ccc tcg agc 221

Lys Phe Gln His Pro Gly Ser Asp Met Arg Gln Glu Lys Pro Ser Ser

10 15 20 25

ccc agc ccg atg cct tcc tcc aca cca agc ccc agc ctg aac cta ggg 269

Pro Ser Pro Met Pro Ser Ser Thr Pro Ser Pro Ser Leu Asn Leu Gly

30 35 40

aac aca gag gag gcc atc cgg gac aac tca cag gtg aac gca gtc acg 317

Asn Thr Glu Glu Ala Ile Arg Asp Asn Ser Gln Val Asn Ala Val Thr

45 50 55

gtg ctc acg ctc ctg gac aag ctg gtg aac atg cta gac gct gtg cag 365

Val Leu Thr Leu Leu Asp Lys Leu Val Asn Met Leu Asp Ala Val Gln
 60 65 70
 gag aac cag cac aag atg gag cag cga cag atc agt ttg gag ggc tcc 413
 Glu Asn Gln His Lys Met Glu Gln Arg Gln Ile Ser Leu Glu Gly Ser
 75 80 85
 gtg aag ggc atc cag aat gac ctc acc aag ctc tcc aag tac cag gcc 461
 Val Lys Gly Ile Gln Asn Asp Leu Thr Lys Leu Ser Lys Tyr Gln Ala
 90 95 100 105
 tcc acc agc aac acg gtg agc aag ctg ctg gag aag tcc cgc aag gtc 509
 Ser Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys Ser Arg Lys Val
 110 115 120
 agc gcc cac acg cgc gcg gtc aaa gag cgc atg gat agg cag tgc gca 557
 Ser Ala His Thr Arg Ala Val Lys Glu Arg Met Asp Arg Gln Cys Ala
 125 130 135
 cag gtg aag cgg ctg gag aac aac cac gcc cag ctc ctc cga cgc aac 605
 Gln Val Lys Arg Leu Glu Asn Asn His Ala Gln Leu Leu Arg Arg Asn
 140 145 150
 cat ttc aaa gtg ctc atc ttc cag gag gaa aat gag atc cct gcc agc 653
 His Phe Lys Val Leu Ile Phe Gln Glu Glu Asn Glu Ile Pro Ala Ser
 155 160 165
 gtg ttt gtg aaa cag ccc gtt tcc ggt gcc gtg gaa ggg aag gag gag 701
 Val Phe Val Lys Gln Pro Val Ser Gly Ala Val Glu Gly Lys Glu Glu
 170 175 180 185
 ctt ccg gat gaa aac aaa tcc ctg gag gaa acc ctg cac acc gtg gac 749
 Leu Pro Asp Glu Asn Lys Ser Leu Glu Glu Thr Leu His Thr Val Asp
 190 195 200

ctc tcc tca gat gat gat ttg ccc cac gat gag gag gcc ctg gaa gac 797
 Leu Ser Ser Asp Asp Asp Leu Pro His Asp Glu Glu Ala Leu Glu Asp
 205 210 215
 agt gcc gag gaa aag gtg gaa gaa agt agg gca gag aaa ata aaa aga 845
 Ser Ala Glu Glu Lys Val Glu Glu Ser Arg Ala Glu Lys Ile Lys Arg
 220 225 230
 tcc agc ctg aag aaa gtg gat agc ctc aag aaa gca ttt tct cgc cag 893
 Ser Ser Leu Lys Lys Val Asp Ser Leu Lys Lys Ala Phe Ser Arg Gln
 235 240 245
 aac atc gag aaa aag atg aac aag ctg ggg aca aag atc gla tct gla 941
 Asn Ile Glu Lys Lys Met Asn Lys Leu Gly Thr Lys Ile Val Ser Val
 250 255 260 265
 gag agg aga gag aag att aag aaa tct ctc acg tca aat cac cag aaa 989
 Glu Arg Arg Glu Lys Ile Lys Lys Ser Leu Thr Ser Asn His Gln Lys
 270 275 280
 ata tcc tca gga aaa agc tcc ccc ttc aag gtt tct ccc ctc act ttc 1037
 Ile Ser Ser Gly Lys Ser Ser Pro Phe Lys Val Ser Pro Leu Thr Phe
 285 290 295
 ggg cgg aag aaa gtc cga gag gga gaa agc cat gca gaa aat gag acc 1085
 Gly Arg Lys Lys Val Arg Glu Gly Glu Ser His Ala Glu Asn Glu Thr
 300 305 310
 aag tca gaa gac ctg cct agc agt gag cag atg cca aat gac cag gaa 1133
 Lys Ser Glu Asp Leu Pro Ser Ser Glu Gln Met Pro Asn Asp Gln Glu
 315 320 325
 gag gag tcc ttt gca gag ggt cat tcc gaa gcg tcc ctc gcc agc gct 1181
 Glu Glu Ser Phe Ala Glu Gly His Ser Glu Ala Ser Leu Ala Ser Ala
 330 335 340 345

ctg gtg gaa ggg gaa att gca gag gag gct gct gag aag gcg acc tcc 1229
 Leu Val Glu Gly Glu Ile Ala Glu Glu Ala Ala Glu Lys Ala Thr Ser
 350 355 360
 agg ggg agl aac tcg ggg atg gac agc aac atc gac ttg act att gtg 1277
 Arg Gly Ser Asn Ser Gly Met Asp Ser Asn Ile Asp Leu Thr Ile Val
 365 370 375
 gaa gat gaa gag gag gag tca gtg gcc ctg gaa cag gca cag aag gta 1325
 Glu Asp Glu Glu Glu Glu Ser Val Ala Leu Glu Gln Ala Gln Lys Val
 380 385 390
 cgc tat gag ggt agc tac gcg cta aca tcc gag gag gcg gag cgc tcc 1373
 Arg Tyr Glu Gly Ser Tyr Ala Leu Thr Ser Glu Glu Ala Glu Arg Ser
 395 400 405
 gat ggg gac ccc gtg cag ccc gcc gtg ctc cag gtg cac cag acc tcc 1421
 Asp Gly Asp Pro Val Gln Pro Ala Val Leu Gln Val His Gln Thr Ser
 410 415 420 425
 tgagcttaga gccaccgtgc catcctgtgc tgtgctcaag cgggcagcca gggctgaaga 1481
 acaaactctt gcacatctcc agcacgactc acccactcct gcgttctgt ccaggcagta 1541
 atcattgacc atatagtcac agtaagacac acgagaccag gctttaccat gaaagcgacc 1601
 tgtcacggac tccactttta atttgccttt aggttctatc tctgtagaat gtctccaaga 1661
 ttgaagaaga aactgagcag ttgaaaaatg ctaatctctt tgacttagtc agaaaaaac 1721
 agaggataat taagatacta gtcatgaaaa gtgattcatt cttttttgtc attccatc 1779

<210> 70

<211> 425

<212> PRT

<213> Homo sapiens

<400> 70

Met Gly Glu Asp Ala Ala Gln Ala Glu Lys Phe Gln His Pro Gly Ser
 1 5 10 15
 Asp Met Arg Gln Glu Lys Pro Ser Ser Pro Ser Pro Met Pro Ser Ser
 20 25 30
 Thr Pro Ser Pro Ser Leu Asn Leu Gly Asn Thr Glu Glu Ala Ile Arg
 35 40 45
 Asp Asn Ser Gln Val Asn Ala Val Thr Val Leu Thr Leu Leu Asp Lys
 50 55 60
 Leu Val Asn Met Leu Asp Ala Val Gln Glu Asn Gln His Lys Met Glu
 65 70 75 80
 Gln Arg Gln Ile Ser Leu Glu Gly Ser Val Lys Gly Ile Gln Asn Asp
 85 90 95
 Leu Thr Lys Leu Ser Lys Tyr Gln Ala Ser Thr Ser Asn Thr Val Ser
 100 105 110
 Lys Leu Leu Glu Lys Ser Arg Lys Val Ser Ala His Thr Arg Ala Val
 115 120 125
 Lys Glu Arg Met Asp Arg Gln Cys Ala Gln Val Lys Arg Leu Glu Asn
 130 135 140
 Asn His Ala Gln Leu Leu Arg Arg Asn His Phe Lys Val Leu Ile Phe
 145 150 155 160
 Gln Glu Glu Asn Glu Ile Pro Ala Ser Val Phe Val Lys Gln Pro Val
 165 170 175
 Ser Gly Ala Val Glu Gly Lys Glu Glu Leu Pro Asp Glu Asn Lys Ser
 180 185 190
 Leu Glu Glu Thr Leu His Thr Val Asp Leu Ser Ser Asp Asp Asp Leu
 195 200 205

Pro His Asp Glu Glu Ala Leu Glu Asp Ser Ala Glu Glu Lys Val Glu
 210 215 220
 Glu Ser Arg Ala Glu Lys Ile Lys Arg Ser Ser Leu Lys Lys Val Asp
 225 230 235 240
 Ser Leu Lys Lys Ala Phe Ser Arg Gln Asn Ile Glu Lys Lys Met Asn
 245 250 255
 Lys Leu Gly Thr Lys Ile Val Ser Val Glu Arg Arg Glu Lys Ile Lys
 260 265 270
 Lys Ser Leu Thr Ser Asn His Gln Lys Ile Ser Ser Gly Lys Ser Ser
 275 280 285
 Pro Phe Lys Val Ser Pro Leu Thr Phe Gly Arg Lys Lys Val Arg Glu
 290 295 300
 Gly Glu Ser His Ala Glu Asn Glu Thr Lys Ser Glu Asp Leu Pro Ser
 305 310 315 320
 Ser Glu Gln Met Pro Asn Asp Gln Glu Glu Glu Ser Phe Ala Glu Gly
 325 330 335
 His Ser Glu Ala Ser Leu Ala Ser Ala Leu Val Glu Gly Glu Ile Ala
 340 345 350
 Glu Glu Ala Ala Glu Lys Ala Thr Ser Arg Gly Ser Asn Ser Gly Met
 355 360 365
 Asp Ser Asn Ile Asp Leu Thr Ile Val Glu Asp Glu Glu Glu Glu Ser
 370 375 380
 Val Ala Leu Glu Gln Ala Gln Lys Val Arg Tyr Glu Gly Ser Tyr Ala
 385 390 395 400
 Leu Thr Ser Glu Glu Ala Glu Arg Ser Asp Gly Asp Pro Val Gln Pro
 405 410 415
 Ala Val Leu Gln Val His Gln Thr Ser

420

425

<210> 71

<211> 2638

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (288).. (1844)

<400> 71

gaggaaaggg gaaatgcggc cegtccecca ctcagtcca ctctgtgcca ctccgtgcca 60
 ggccctgagg gcacccgggt gtgtcttct tccgtcttc cccaaggact atcagagatg 120
 ccagcgtgac cctgacacg tgtgtgcagc agcctgcagc tgccccaagc catggctgaa 180
 cactgactcc cagctgtggg cttcaccatt acagactccc cagggttca aagacttctc 240
 agcttcgagc atggcttttg gctgtcaggg cagctgtaca atagtgg atg ttt gag 296

Met Phe Glu

I

acg gag gca gat gag aag agg gag atg gcc ttg gag gaa ggg aag ggg 344

Thr Glu Ala Asp Glu Lys Arg Glu Met Ala Leu Glu Glu Gly Lys Gly

5

10

15

cct ggt gcc gag gat tcc cca ccc agc aag gag ccc tct cct ggc cag 392

Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser Pro Gly Gln

20

25

30

35

gag ctt cct cca gga caa gac ctt cca ccc aac aag gac tcc cct tct 440

Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp Ser Pro Ser

40

45

50

ggg cag gaa ccc gct ccc agc caa gaa cca ctg tcc agc aaa gac tca 488

Gly Gln Glu Pro Ala Pro Ser Gln Glu Pro Leu Ser Ser Lys Asp Ser
 55 60 65
 gct acc tct gaa gga tcc cct cca ggc cca gat gct ccg ccc agc aag 536
 Ala Thr Ser Glu Gly Ser Pro Pro Gly Pro Asp Ala Pro Pro Ser Lys
 70 75 80
 gat gtg cca cca tgc cag gaa ccc cct cca gcc caa gac ctc tca ccc 584
 Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp Leu Ser Pro
 85 90 95
 tgc cag gac cta cct gct ggt caa gaa ccc ctg cct cac cag gac cct 632
 Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His Gln Asp Pro
 100 105 110 115
 cta ctc acc aaa gac ctc cct gcc atc cag gaa tcc ccc acc cgg gac 680
 Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro Thr Arg Asp
 120 125 130
 ctt cca ccc tgt caa gat ctg cct cct agc cag gtc tcc ctg cca gcc 728
 Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser Leu Pro Ala
 135 140 145
 aag gcc ctt act gag gac acc atg agc tcc ggg gac cta cta gca gct 776
 Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu Leu Ala Ala
 150 155 160
 act ggg gac cca cct gcg gcc ccc agg cca gcc ttc gtg atc cct gag 824
 Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val Ile Pro Glu
 165 170 175
 gtc cgg ctg gat agc acc tac agc cag aag gca ggg gca gag cag ggc 872
 Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala Glu Gln Gly
 180 185 190 195

tgc tgc gga gat gag gag gat gca gaa gag gcc gag gag glg gag gag	920
Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu Val Glu Glu	
200 205 210	
ggg gag gaa ggg gag gag gac gag gat gag gac acc agc gat gac aac	968
Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser Asp Asp Asn	
215 220 225	
tac gga gag cgc agt gag gcc aag cgc agc agc atg atc gag acg ggc	1016
Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile Glu Thr Gly	
230 235 240	
cag ggg gct gag ggt ggc ctc tca ctg cgt glg cag aac tgc ctg cgg	1064
Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn Ser Leu Arg	
245 250 255	
cgc cgg acg cac agc gag ggc agc ctg ctg cag gag ccc cga ggg ccc	1112
Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro Arg Gly Pro	
260 265 270 275	
tgc ttt gcc tcc gac acc acc ttg cac tgc tca gac ggt gag ggc gcc	1160
Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly Glu Gly Ala	
280 285 290	
gcc tcc acc tgg ggc atg cct tgc ccc agc acc ctc aag aaa gag ctg	1208
Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys Lys Glu Leu	
295 300 305	
ggc cgc aat ggt ggc tcc atg cac cac ctt tcc ctc ttc ttc aca gga	1256
Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe Phe Thr Gly	
310 315 320	
cac agg aag atg agc ggg gct gac acc gtt ggg gat gat gac gaa gcc	1304
His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp Asp Glu Ala	
325 330 335	

tcc cgg aag aga aag agc aaa aac cta gcc aag gac atg aag aac aag 1352
 Ser Arg Lys Arg Lys Ser Lys Asn Leu Ala Lys Asp Met Lys Asn Lys
 340 345 350 355
 ctg ggg atc ttc aga cgg cgg aat gag tcc cct gga gcc cct ccc gcg 1400
 Leu Gly Ile Phe Arg Arg Arg Asn Glu Ser Pro Gly Ala Pro Pro Ala
 360 365 370
 ggc aag gca gac aaa atg atg aag tca ttc aag ccc acc tca gag gaa 1448
 Gly Lys Ala Asp Lys Met Met Lys Ser Phe Lys Pro Thr Ser Glu Glu
 375 380 385
 gcc ctc aag tgg ggc gag tcc ttg gag aag ctg ctg gtt cac aaa tac 1496
 Ala Leu Lys Trp Gly Glu Ser Leu Glu Lys Leu Leu Val His Lys Tyr
 390 395 400
 ggg tta gca gtg ttc caa gcc ttc ctt cgc act gag ttc agt gag gag 1544
 Gly Leu Ala Val Phe Gln Ala Phe Leu Arg Thr Glu Phe Ser Glu Glu
 405 410 415
 aat ctg gag ttc tgg ttg gct tgt gag gac ttc aag aag gtc aag tca 1592
 Asn Leu Glu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys Val Lys Ser
 420 425 430 435
 cag tcc aag atg gca tcc aag gcc aag aag atc ttt gct gaa tac atc 1640
 Gln Ser Lys Met Ala Ser Lys Ala Lys Lys Ile Phe Ala Glu Tyr Ile
 440 445 450
 gcg atc cag gca tgc aag gag gtc aac ctg gac tcc tac acg cgg gag 1688
 Ala Ile Gln Ala Cys Lys Glu Val Asn Leu Asp Ser Tyr Thr Arg Glu
 455 460 465
 cac acc aag gac aac ctg cag agc gtc acg cgg ggc tgc ttc gac ctg 1736
 His Thr Lys Asp Asn Leu Gln Ser Val Thr Arg Gly Cys Phe Asp Leu

470	475	480	
gca cag aag cgc atc ttc ggg ctc atg gaa aag gac tgc tac cct cgc			1784
Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser Tyr Pro Arg			
485	490	495	
ttt ctc cgt tct gac ctc tac ctg gac ctt att aac cag aag aag atg			1832
Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln Lys Lys Met			
500	505	510	515
agt ccc ccg ctt taggggccac tggagtcgag ctacagcgttc acaccaggcg			1884
Ser Pro Pro Leu			
ggctgggtcc cctgccacc tgcctccctg cccctctga cggagggggc aagcaagccc			1944
ccagaggccg tgtctctgga cagacggata gacatacgga agcgaggcct ggaccaagag			2004
aggcccaggc tactggagga gtagaaggat gggccccgtg gggccccac tgccccggtg			2064
cgagggggcc caagaccctg gcaggtcagg ggccctggcc aagccagatc tggagctgct			2124
gtccctgct gcggagaccg cggaggttc gcgttgacca agttccttaa agaactggct			2184
gatggggcag gaggtccagg cctgggcctt cgggcccctc tagagggcca ttggagcttg			2244
cagctcagac ccccacttg agtittatit atttaaata tagttggatg cttggcacgt			2304
cgctctgtaa taggaaacct ttgcctcacc agttttctg attacaagt gcaatatit			2364
agccaatgcc ttgggagaag ctgccatgca aaggtggaca ccattctcca gcttcagggg			2424
atatgtctgt cccgggcacc gg'ggcaggc agctggcctt ctggactaag gcagcctggg			2484
gggacactgc agtctggcta cacacagaga tctggcacc cctgggtgga gtgtccctcg			2544
ggggcttttg gaaagcatgg caccctcaga ccacacagta gccaaagtct ggagcaaata			2604
aaaggccctg gtattttctt gtcttgaaa aaaa			2638

<210> 72

<211> 519

<212> PRT

<213> Homo sapiens

<400> 72

Met Phe Glu Thr Glu Ala Asp Glu Lys Arg Glu Met Ala Leu Glu Glu

1 5 10 15

Gly Lys Gly Pro Gly Ala Glu Asp Ser Pro Pro Ser Lys Glu Pro Ser

20 25 30

Pro Gly Gln Glu Leu Pro Pro Gly Gln Asp Leu Pro Pro Asn Lys Asp

35 40 45

Ser Pro Ser Gly Gln Glu Pro Ala Pro Ser Gln Glu Pro Leu Ser Ser

50 55 60

Lys Asp Ser Ala Thr Ser Glu Gly Ser Pro Pro Gly Pro Asp Ala Pro

65 70 75 80

Pro Ser Lys Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp

85 90 95

Leu Ser Pro Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His

100 105 110

Gln Asp Pro Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro

115 120 125

Thr Arg Asp Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser

130 135 140

Leu Pro Ala Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu

145 150 155 160

Leu Ala Ala Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val

165 170 175

Ile Pro Glu Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala

180 185 190

Glu Gln Gly Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu

195 200 205

Val Glu Glu Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser
 210 215 220
 Asp Asp Asn Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile
 225 230 235 240
 Glu Thr Gly Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn
 245 250 255
 Ser Leu Arg Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro
 260 265 270
 Arg Gly Pro Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly
 275 280 285
 Glu Gly Ala Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys
 290 295 300
 Lys Glu Leu Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe
 305 310 315 320
 Phe Thr Gly His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp
 325 330 335
 Asp Glu Ala Ser Arg Lys Arg Lys Ser Lys Asn Leu Ala Lys Asp Met
 340 345 350
 Lys Asn Lys Leu Gly Ile Phe Arg Arg Arg Asn Glu Ser Pro Gly Ala
 355 360 365
 Pro Pro Ala Gly Lys Ala Asp Lys Met Met Lys Ser Phe Lys Pro Thr
 370 375 380
 Ser Glu Glu Ala Leu Lys Trp Gly Glu Ser Leu Glu Lys Leu Leu Val
 385 390 395 400
 His Lys Tyr Gly Leu Ala Val Phe Gln Ala Phe Leu Arg Thr Glu Phe
 405 410 415

Ser Glu Glu Asn Leu Glu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys

420

425

430

Val Lys Ser Gln Ser Lys Met Ala Ser Lys Ala Lys Lys Ile Phe Ala

435

440

445

Glu Tyr Ile Ala Ile Gln Ala Cys Lys Glu Val Asn Leu Asp Ser Tyr

450

455

460

Thr Arg Glu His Thr Lys Asp Asn Leu Gln Ser Val Thr Arg Gly Cys

465

470

475

480

Phe Asp Leu Ala Gln Lys Arg Ile Phe Gly Leu Met Glu Lys Asp Ser

485

490

495

Tyr Pro Arg Phe Leu Arg Ser Asp Leu Tyr Leu Asp Leu Ile Asn Gln

500

505

510

Lys Lys Met Ser Pro Pro Leu

515

<210> 73

<211> 1901

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (250).. (1206)

<400> 73

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 gtcccagggt tggaagatta tctcaccggg ccccagctat ataagctgac cgggtgtggag 180
 gggcccagca gggccaactc cagggatctc ttcacgaca gaaaaacata caagactcct 240

tcagccaac atg atg gta ctg aaa gta gag gaa ctg gtc act gga aag aag 291

Met Met Val Leu Lys Val Glu Glu Leu Val Thr Gly Lys Lys

1

5

10

aat ggc aat ggg gag gca ggg gaa ttc ctt cct gag gat ttc aga gat 339

Asn Gly Asn Gly Glu Ala Gly Glu Phe Leu Pro Glu Asp Phe Arg Asp

15

20

25

30

gga gag tat gaa gct gct gtt act tta gag aag cag gag gat ctg aag 387

Gly Glu Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys

35

40

45

aca ctt cta gcc cac cct gtg acc ctg ggg gag caa cag tgg aaa agc 435

Thr Leu Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser

50

55

60

gag aaa caa cga gag gca gag ctg cca aag aaa aaa cta gaa caa aga 483

Glu Lys Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg

65

70

75

tcc aag ctt gaa aat tta gaa gac ctt gaa ata atc att caa ctg aag 531

Ser Lys Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys

80

85

90

aaa agg aaa aaa tac agg aaa act aaa gtt cca gtt gta aag gaa cca 579

Lys Arg Lys Lys Tyr Arg Lys Thr Lys Val Pro Val Val Lys Glu Pro

95

100

105

110

gaa cct gaa atc att acg gaa cct gtg gat gtg cct acg ttt ctg aag 627

Glu Pro Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys

115

120

125

gct gct ctg gag aat aaa ctg cca gla gta gaa aaa ttc ttg tca gac 675

Ala Ala Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp

130

135

140

aag aac aat cca gat gtt tgt gat gag tat aaa cgg aca gct ctt cat 723
 Lys Asn Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His
 145 150 155
 aga gca tgc ttg gaa gga cat ttg gca att gtg gag aag tta atg gaa 771
 Arg Ala Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu
 160 165 170
 gct gga gcc cag atc gaa ttc cgt gat atg ctt gaa tcc aca gcc atc 819
 Ala Gly Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile
 175 180 185 190
 cac tgg gca agc cgt gga gga aac ctg gat gtt tta aaa ttg ttg ctg 867
 His Trp Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu
 195 200 205
 aat aaa gga gca aaa att agc gcc cga gat aag ttg ctc agc aca gcg 915
 Asn Lys Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala
 210 215 220
 ctg cat gtg gcg gtg agg act ggc cac tat gag tgc gcg gag cat ctt 963
 Leu His Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu
 225 230 235
 atc gcc tgt gag gca gac ctc aac gcc aaa gac aga gaa gga gat acc 1011
 Ile Ala Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr
 240 245 250
 ccg ttg cat gat gcg gtg aga ctg aac cgc tat aag atg atc cga ctc 1059
 Pro Leu His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu
 255 260 265 270
 ctg att atg tat ggc gcg gat ctc aac atc aag aac tgt gct ggg aag 1107
 Leu Ile Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys

275	280	285	
acg ccg atg gat ctg gtg cta cac tgg cag aat gga acc aaa gca ata			1155
Thr Pro Met Asp Leu Val Leu His Trp Gln Asn Gly Thr Lys Ala Ile			
290	295	300	
ttc gac agc ctc aga gag aac tcc tac aag acc tct cgc ata gct aca			1203
Phe Asp Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr			
305	310	315	
ttc tgaggcaaac gacagactct taatcagtaa atgttcactg gcattitgaa			1256
Phe			
ggcatggccc aggagaagag acactagcca taaaatctag ttictattta tcaacgtgtt			1316
glgaagaatgt acctaatgaa gttitgagaa agcacagggt tataggigt taaatttcct			1376
ttagtgaaac tcttatttat ttttatgtat tcttgittat ttatttactg ccacgtact			1436
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ttcagagcct tcccacccat aggtagtctt taaaccaggi gaaagagcaa agttcaagt			1556
cctactttatg tgcatttcgc tcatgtaaga gttitttaaga gagggctgat taccacagcc			1616
ctctttttct cigaattttt aatgcagaag ttgaaatgaa gcaagggaag gcatgtagg			1676
acaggaaagg aaacaatgga aggaaagtga ttctgtgaaa aggacagtga agccagctat			1736
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agagtaccca agtgaagaga acgtcatgag tgtaagtgca aatcagtgga aggagcggca			1856
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<210> 74

<211> 319

<212> PRT

<213> Homo sapiens

<400> 74

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Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys Thr Leu			
35	40	45	
Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser Glu Lys			
50	55	60	
Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg Ser Lys			
65	70	75	80
Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys Lys Arg			
85	90	95	
Lys Lys Tyr Arg Lys Thr Lys Val Pro Val Val Lys Glu Pro Glu Pro			
100	105	110	
Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys Ala Ala			
115	120	125	
Leu Glu Asn Lys Leu Pro Val Val Glu Lys Phe Leu Ser Asp Lys Asn			
130	135	140	
Asn Pro Asp Val Cys Asp Glu Tyr Lys Arg Thr Ala Leu His Arg Ala			
145	150	155	160
Cys Leu Glu Gly His Leu Ala Ile Val Glu Lys Leu Met Glu Ala Gly			
165	170	175	
Ala Gln Ile Glu Phe Arg Asp Met Leu Glu Ser Thr Ala Ile His Trp			
180	185	190	
Ala Ser Arg Gly Gly Asn Leu Asp Val Leu Lys Leu Leu Leu Asn Lys			
195	200	205	
Gly Ala Lys Ile Ser Ala Arg Asp Lys Leu Leu Ser Thr Ala Leu His			
210	215	220	

Val Ala Val Arg Thr Gly His Tyr Glu Cys Ala Glu His Leu Ile Ala

225 230 235 240

Cys Glu Ala Asp Leu Asn Ala Lys Asp Arg Glu Gly Asp Thr Pro Leu

245 250 255

His Asp Ala Val Arg Leu Asn Arg Tyr Lys Met Ile Arg Leu Leu Ile

260 265 270

Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys Thr Pro

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Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr Phe

305 310 315

<210> 75

<211> 5613

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118).. (5475)

<400> 75

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atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta gcc ctg tgc aga 165

Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg

1 5 10 15

gcc cga gtg cgc gct cag gaa ccc gag ttc agc tac ggc tgc gca gaa 213

Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
 20 25 30
 ggc agc tgc tat ccc gcc acg ggc gac ctt ctc atc ggc cga gca cag 261
 Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
 35 40 45
 aag ctt tgc gtg acc tgc acg tgc ggg ctg cac aag ccc gaa ccc tac 309
 Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
 50 55 60
 tgt atc gtc agc cac ttg cag gag gac aaa aaa tgc ttc ata tgc aat 357
 Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn
 65 70 75 80
 tcc caa gat cct tat cat gag acc ctg aat cct gac agc cat ctc att 405
 Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
 85 90 95
 gaa aat gtg gtc act aca ttt gct cca aac cgc ctt aag att tgg tgg 453
 Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
 100 105 110
 caa tct gaa aat ggt gtg gaa aat gta act atc caa ctg gat ttg gaa 501
 Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
 115 120 125
 gca gaa ttc cat ttt act cat ctc ata atg act ttc aag aca ttc cgt 549
 Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
 130 135 140
 cca gct gct atg ctg ata gaa cga tgc tcc gac ttt ggg aaa acc tgg 597
 Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
 145 150 155 160

ggt gtg tat aga tac ttc gcc tat gac tgt gag gcc tcg ttt cca ggc 645
 Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly
 165 170 175
 att tca act ggc ccc atg aaa aaa gtc gat gac ata att tgt gat tct 693
 Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
 180 185 190
 cga tat tct gac att gaa ccc tca act gaa gga gag gtg ata ttt cgt 741
 Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
 195 200 205
 gct tta gat cct gct ttc aaa ata gaa gat cct tat agc cca agg ata 789
 Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
 210 215 220
 cag aat tta tta aaa att acc aac ttg aga atc aag ttt gtg aaa ctg 837
 Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
 225 230 235 240
 cat act ttg gga gat aac ctt ctg gat tcc agg atg gaa atc aga gaa 885
 His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
 245 250 255
 aag tat tat tat gca gtt tat gat atg gtg gtt cga gga aat tgc ttc 933
 Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
 260 265 270
 tgc tat ggt cat gcc agc gaa tgt gcc cct gtc gat gga ttc aat gaa 981
 Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu
 275 280 285
 gaa gtg gaa gga atg gtt cac gga cac tgc atg tgc agg cat aac acc 1029
 Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
 290 295 300

aag ggc tta aac tgt gaa ctc tgc atg gat ttc tac cat gat tta cct 1077
 Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
 305 310 315 320
 tgg aga cct gct gaa ggc cga aac agc aac gcc tgt aaa aaa tgt aac 1125
 Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
 325 330 335
 tgc aat gaa cat tcc atc tct tgt cac ttt gac atg gct gtt tac ctg 1173
 Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu
 340 345 350
 gcc acg ggg aac gtc agc gga ggc gtg tgt gat gac tgt cag cac aac 1221
 Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn
 355 360 365
 acc atg ggg cgc aac tgt gag cag tgc aag ccg ttt tac tac cag cac 1269
 Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His
 370 375 380
 cca gag agg gac atc cga gat cct aat ttc tgt gaa cga tgt acg tgt 1317
 Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys
 385 390 395 400
 gac cca gct ggc tct caa aat gag gga att tgt gac agc tat act gat 1365
 Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp
 405 410 415
 ttt tct act ggt ctc att gct ggc cag tgt cgg tgt aaa tta aat gtg 1413
 Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val
 420 425 430
 gaa gga gaa cat tgt gat gtt tgc aaa gaa ggc ttc tat gat tta agc 1461
 Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser

435	440	445	
agt gaa gat cca ttt ggt tgt aaa tct tgt gct tgc aat cct ctg gga	1509		
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly			
450	455	460	
aca att cct gga ggg aat cct tgt gat tcc gag aca ggt cac tgc tac	1557		
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr			
465	470	475	480
tgc aag cgt ctg glg aca gga cag cat tgt gac cag tgc ctg cca gag	1605		
Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu			
485	490	495	
cac tgg ggc tta agc aat gat ttg gat gga tgt cga cca tgt gac tgt	1653		
His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys			
500	505	510	
gac ctt ggg gga gcc tta aac aac agt tgc ttt gcg gag tca ggc cag	1701		
Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln			
515	520	525	
tgc tca tgc cgg cct cac atg att gga cgt cag tgc aac gaa gtg gaa	1749		
Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu			
530	535	540	
cct ggt tac tac ttt gcc acc ctg gat cac tac ctc tat gaa gcg gag	1797		
Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu			
545	550	555	560
gaa gcc aac ttg ggg cct ggg gtt agc ata gtg gag cgg caa tat atc	1845		
Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile			
565	570	575	
cag gac cgg att ccc tcc tgg act gga gcc ggc ttc gtc cga gtg cct	1893		
Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro			

580	585	590	
gaa ggg gct tat ttg gag ttt ttc att gac aac ata cca tat tcc atg			1941
Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met			
595	600	605	
gag tac gac atc cta att cgc tac gag cca cag cta ccc gac cac tgg			1989
Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp			
610	615	620	
gaa aaa gct gtc atc aca gtg cag cga cct gga agg att cca acc agc			2037
Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser			
625	630	635	640
agc cga tgt ggt aat acc atc ccc gat gat gac aac cag gtg gtg tca			2085
Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser			
645	650	655	
tta tca cca ggc tca aga tat gtc gtc ctt cct cgg ccg gtg tgc ttt			2133
Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe			
660	665	670	
gag aag gga aca aac tac acg gtg agg ttg gag ctg cct cag tac acc			2181
Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr			
675	680	685	
tcc tct gat agc gac gtg gag agc ccc tac acg ctg atc gat tct ctt			2229
Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu			
690	695	700	
gtt ctc atg cca tac tgt aaa tca ctg gac atc ttc acc gtg gga ggt			2277
Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly			
705	710	715	720
tca gga gat ggg gtg gtc acc aac agt gcc tgg gaa acc ttt cag aga			2325

Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg

725

730

735

tac cga tgt cta gag aac agc aga agc gtt gtg aaa aca ccg atg aca 2373

Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr

740

745

750

gat gtt tgc aga aac atc atc ttt agc att tct gcc ctg tta cac cag 2421

Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln

755

760

765

aca ggc ctg gct tgt gaa tgc gac cct cag ggt tgc tta agt tcc gtg 2469

Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val

770

775

780

tgt gat ccc aac gga ggc cag tgc cag tgc cgg ccc aac gtg gtt gga 2517

Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly

785

790

795

800

aga acc tgc aac aga tgt gca cct gga act ttt ggc ttt ggc ccc agt 2565

Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser

805

810

815

gga tgc aaa cct tgt gag tgc cat ctg caa gga tct gtc aat gcc ttc 2613

Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe

820

825

830

tgc aat ccc gtc act ggc cag tgc cac tgt ttc cag gga gtg tat gct 2661

Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala

835

840

845

cgg cag tgt gat cgg tgc tta cct ggg cac tgg ggc ttt cca agt tgc 2709

Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys

850

855

860

cag ccc tgc cag tgc aat ggc cac gcc gat gac tgc gac cca gtg act 2757

Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr
 865 870 875 880
 ggg gag tgc ttg aac tgc cag gac tac acc atg ggt cat aac tgt gaa 2805
 Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu
 885 890 895
 agg tgc ttg gct ggt tac tat ggc gac ccc atc att ggg tca ggt gat 2853
 Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
 900 905 910
 cac tgc cgc cct tgc cct tgc cca gat ggt ccc gac agt gga cgc cag 2901
 His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
 915 920 925
 ttt gcc agg agc tgc tac caa gat cct gtt act tta cag ctt gcc tgt 2949
 Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
 930 935 940
 gtt tgt gat cct gga tac att ggt tcc aga tgt gac gac tgt gcc tca 2997
 Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
 945 950 955 960
 gga tac ttt ggc aat cca tca gaa gtt ggg ggg tcg tgt cag cct tgc 3045
 Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys
 965 970 975
 cag tgt cac aac aac att gac acg aca gac cca gaa gcc tgt gac aag 3093
 Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
 980 985 990
 gag act ggg agg tgt ctc aag tgc ctg tac cac acg gaa ggg gaa cac 3141
 Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His
 995 1000 1005

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 Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp
 1010 1015 1020
 tgt cga aag tgt gtc tgt aat tac ctg ggc acc gtg caa gag cac tgt 3237
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 1045 1050 1055
 ctt cct aat gtg atc ggg cag aac tgt gac cgc tgt gcg ccc aat acc 3333
 Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr
 1060 1065 1070
 tgg cag ctg gcc agt ggc act ggc tgt gac cca tgc aac tgc aat gct 3381
 Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala
 1075 1080 1085
 gct cat tcc ttc ggg cca tct tgc aat gag ttc acg ggg cag tgc cag 3429
 Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln
 1090 1095 1100
 tgc atg cct ggg ttt gga ggc cgc acc tgc agc gag tgc cag gaa ctc 3477
 Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu
 1105 1110 1115 1120
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 Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro
 1125 1130 1135
 agg ggc att gag acg cca cag tgt gac cag tcc acg ggc cag tgt gtc 3573
 Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val
 1140 1145 1150

tgc gtt gag ggt gtt gag ggt cca cgc tgt gac aag tgc acg cga ggg 3621
 Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly
 1155 1160 1165
 tac tcg ggg gtc ttc cct gac tgc aca ccc tgc cac cag tgc ttt gct 3669
 Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala
 1170 1175 1180
 ctc tgg gat gtg atc att gcc gag ctg acc aac agg aca cac aga ttc 3717
 Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe
 1185 1190 1195 1200
 ctg gag aaa gcc aag gcc ttg aag atc agt ggt gtg atc ggg cct tac 3765
 Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr
 1205 1210 1215
 cgt gag act gtg gac tcg gtg gag agg aaa gtc agc gag ata aaa gac 3813
 Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp
 1220 1225 1230
 atc ctg gcg cag agc ccc gca gca gag cca ctg aaa aac att ggg aat 3861
 Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn
 1235 1240 1245
 ctc ttt gag gaa gca gag aaa ctg att aaa gat gtt aca gaa atg atg 3909
 Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met
 1250 1255 1260
 gct caa gla gaa gtg aaa tta tct gac aca act tcc caa agc aac agc 3957
 Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser
 1265 1270 1275 1280
 aca gcc aaa gaa ctg gat tct cta cag aca gaa gcc gaa agc cta gac 4005
 Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp

1285	1290	1295	
aac act gtg aaa gaa ctt gct gaa caa ctg gaa ttt atc aaa aac tca			4053
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser			
1300	1305	1310	
gat att cgg ggt gcc ttg gat agc att acc aag tat ttc cag atg tct			4101
Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser			
1315	1320	1325	
ctt gag gca gag gag agg gtg aat gcc tcc acc aca gaa ccc aac agc			4149
Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser			
1330	1335	1340	
act gtg gag cag tca gcc ctc atg aga gac aga gta gaa gac gtg atg			4197
Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met			
1345	1350	1355	1360
atg gag cga gaa tcc cag ttc aag gaa aaa caa gag gag cag gct cgc			4245
Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg			
1365	1370	1375	
ctc ctt gat gaa ctg gca ggc aag cta caa agc cta gac ctt tca gcc			4293
Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala			
1380	1385	1390	
gct gcc gaa atg acc tgt gga aca ccc cca ggg gcc tcc tgt tcc gag			4341
Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu			
1395	1400	1405	
act gaa tgt ggc ggg cca aac tgc aga act gac gaa gga gag agg aag			4389
Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys			
1410	1415	1420	
tgt ggg ggg cct ggc tgt ggt ggt ctg gtt act gtt gca cac aac gcc			4437
Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala			

1425	1430	1435	1440	
tgg cag aaa gcc atg gac ttg gac caa gat gtc ctg agt gcc ctg gct				4485
Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala				
	1445	1450	1455	
	gaa gtg gaa cag ctc tcc aag atg gtc tct gaa gca aaa ctg agg gca			4533
	Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala			
	1460	1465	1470	
	gat gag gca aaa caa agt gct gaa gac att ctg ttg aag aca aat gct			4581
	Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala			
	1475	1480	1485	
	acc aaa gaa aaa atg gac aag agc aat gag gag ctg aga aat cta atc			4629
	Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile			
	1490	1495	1500	
	aag caa atc aga aac ttt ttg acc cag gat agt gct gat ttg gac agc			4677
	Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser			
1505	1510	1515	1520	
att gaa gca gtt gct aat gaa gta ttg aaa atg gag atg cct agc acc				4725
Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr				
	1525	1530	1535	
	cca cag cag tta cag aac ttg aca gaa gat ata cgt gaa cga gtt gaa			4773
	Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu			
	1540	1545	1550	
	agc ctt tct caa gta gag gtt att ctt cag cat agt gct gct gac att			4821
	Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile			
	1555	1560	1565	
	gcc aga gct gag atg ttg tta gaa gaa gct aaa aga gca agc aaa agt			4869

Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser

1570

1575

1580

gca aca gat gtt aaa gtc act gca gat atg gta aag gaa gct ctg gaa 4917

Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu

1585

1590

1595

1600

gaa gca gaa aag gcc cag gtc gca gca gag aag gca att aaa caa gca 4965

Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala

1605

1610

1615

gat gaa gac att caa gga acc cag aac ctg tta act tcg att gag tct 5013

Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser

1620

1625

1630

gaa aca gca gct tct gag gaa acc ttg ttc aac gcg tcc cag cgc atc 5061

Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile

1635

1640

1645

agc gag tta gag agg aat gtg gaa gaa ctt aag cgg aaa gct gcc caa 5109

Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln

1650

1655

1660

aac tcc ggg gag gca gaa tat att gaa aaa gta gta tat act gtg aag 5157

Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys

1665

1670

1675

1680

caa agt gca gaa gat gtt aag aag act tta gat ggt gaa ctt gat gaa 5205

Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu

1685

1690

1695

aag tat aaa aaa gta gaa aat tta att gcc aaa aaa act gaa gag tca 5253

Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser

1700

1705

1710

gct gat gcc aga agg aaa gcc gaa atg cta caa aat gaa gca aaa act 5301

Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr

1715

1720

1725

ctt tta gct caa gca aat agc aag ctg caa ctg ctc aaa gat tta gaa 5349

Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu

1730

1735

1740

aga aaa tat gaa gac aat caa aga tac tta gaa gat aaa gct caa gaa 5397

Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu

1745

1750

1755

1760

tta gca aga ctg gaa gga gaa gtc cgt tca ctc cta aag gat ata agc 5445

Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser

1765

1770

1775

cag aaa gii gct gig tat agc aca tgc ttg taacagagga gaataaaaaa 5495

Gln Lys Val Ala Val Tyr Ser Thr Cys Leu

1780

1785

tggctgaggt gaacaaggta aaacaaciac attttaaaaa ctgacttaat gctcttcaaa 5555

ataaaacatc acctatttaa tgtttttaat cacatittgt atgagttaaa taaagccc 5613

<210> 76

<211> 1786

<212> PRT

<213> Homo sapiens

<400> 76

Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg

1

5

10

15

Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu

20

25

30

Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln

35	40	45	
Lys	Leu	Ser	Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
50	55	60	
Cys	Ile	Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn	
65	70	75	80
Ser	Gln	Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile	
85	90	95	
Glu	Asn	Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp	
100	105	110	
Gln	Ser	Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu	
115	120	125	
Ala	Glu	Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg	
130	135	140	
Pro	Ala	Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp	
145	150	155	160
Gly	Val	Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly	
165	170	175	
Ile	Ser	Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser	
180	185	190	
Arg	Tyr	Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg	
195	200	205	
Ala	Leu	Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile	
210	215	220	
Gln	Asn	Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu	
225	230	235	240
His	Thr	Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu	

245	250	255	
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe			
260	265	270	
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu			
275	280	285	
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr			
290	295	300	
Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro			
305	310	315	320
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn			
325	330	335	
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu			
340	345	350	
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn			
355	360	365	
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His			
370	375	380	
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys			
385	390	395	400
Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp			
405	410	415	
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val			
420	425	430	
Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser			
435	440	445	
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly			
450	455	460	

Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr
 465 470 475 480
 Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu
 485 490 495
 His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
 500 505 510
 Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln
 515 520 525
 Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
 530 535 540
 Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu
 545 550 555 560
 Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile
 565 570 575
 Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro
 580 585 590
 Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
 595 600 605
 Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
 610 615 620
 Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser
 625 630 635 640
 Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser
 645 650 655
 Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
 660 665 670

Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
 675 680 685
 Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu
 690 695 700
 Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
 705 710 715 720
 Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
 725 730 735
 Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
 740 745 750
 Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln
 755 760 765
 Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
 770 775 780
 Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
 785 790 795 800
 Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser
 805 810 815
 Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe
 820 825 830
 Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala
 835 840 845
 Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys
 850 855 860
 Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr
 865 870 875 880
 Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu

885	890	895	
Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp			
900	905	910	
His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln			
915	920	925	
Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys			
930	935	940	
Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser			
945	950	955	960
Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys			
965	970	975	
Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys			
980	985	990	
Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His			
995	1000	1005	
Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp			
1010	1015	1020	
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys			
1025	1030	1035	1040
Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys			
1045	1050	1055	
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr			
1060	1065	1070	
Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala			
1075	1080	1085	
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln			

1090	1095	1100	
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu			
1105	1110	1115	1120
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro			
	1125	1130	1135
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val			
	1140	1145	1150
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly			
	1155	1160	1165
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala			
	1170	1175	1180
Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe			
1185	1190	1195	1200
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr			
	1205	1210	1215
Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp			
	1220	1225	1230
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn			
	1235	1240	1245
Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met			
	1250	1255	1260
Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser			
1265	1270	1275	1280
Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp			
	1285	1290	1295
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser			
	1300	1305	1310

Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
 1315 1320 1325
 Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser
 1330 1335 1340
 Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met
 1345 1350 1355 1360
 Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg
 1365 1370 1375
 Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
 1380 1385 1390
 Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu
 1395 1400 1405
 Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys
 1410 1415 1420
 Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala
 1425 1430 1435 1440
 Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala
 1445 1450 1455
 Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala
 1460 1465 1470
 Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala
 1475 1480 1485
 Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile
 1490 1495 1500
 Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser
 1505 1510 1515 1520

Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr
 1525 1530 1535
 Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
 1540 1545 1550
 Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile
 1555 1560 1565
 Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
 1570 1575 1580
 Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
 1585 1590 1595 1600
 Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
 1605 1610 1615
 Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
 1620 1625 1630
 Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile
 1635 1640 1645
 Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
 1650 1655 1660
 Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys
 1665 1670 1675 1680
 Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
 1685 1690 1695
 Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser
 1700 1705 1710
 Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr
 1715 1720 1725
 Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu

1730 1735 1740
 Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu
 1745 1750 1755 1760
 Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
 1765 1770 1775
 Gln Lys Val Ala Val Tyr Ser Thr Cys Leu
 1780 1785

<210> 77

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (27).. (335)

<400> 77

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Met Lys Ser Leu Ile Leu Leu Ala Ile

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ctg gcc gcc tta gcg gta gla act ttg tgt tat gaa tca cat gaa agc 101

Leu Ala Ala Leu Ala Val Val Thr Leu Cys Tyr Glu Ser His Glu Ser

10

15

20

25

atg gaa tct tat gaa ctt aat ccc ttc att aac agg aga aat gca aat 149

Met Glu Ser Tyr Glu Leu Asn Pro Phe Ile Asn Arg Arg Asn Ala Asn

30

35

40

acc ttc ata tcc cct cag cag aga tgg aga gct aaa gtc caa gag agg 197

Thr Phe Ile Ser Pro Gln Gln Arg Trp Arg Ala Lys Val Gln Glu Arg

45	50	55	
atc cga gaa cgc tct aag cct gtc cac gag ctc aat agg gaa gcc tgt	245		
Ile Arg Glu Arg Ser Lys Pro Val His Glu Leu Asn Arg Glu Ala Cys			
60	65	70	
gat gac tac aga ctt tgc gaa cgc tac gcc atg gtt tat gga tac aat	293		
Asp Asp Tyr Arg Leu Cys Glu Arg Tyr Ala Met Val Tyr Gly Tyr Asn			
75	80	85	
gct gcc tat aat cgc tac ttc agg aag cgc cga ggg acc aaa	335		
Ala Ala Tyr Asn Arg Tyr Phe Arg Lys Arg Arg Gly Thr Lys			
90	95	100	
tgagactgag ggaagaaaaa aaatctcttt tttctcggag gctggcacct gatittgtat	395		
ccccctgtag cagcattact gaaatacata ggcttatata caatgcttct ttcctgtata	455		
ttctcttgtc tggctgcacc cctttttccc gccccagat tgataagtaa tgaaagtgca	515		
ctgcagtgag ggtaaagga gagtcaacat atgtgattgt tccataataa acttctgggtg	575		
tgataactttc	585		

<210> 78

<211> 103

<212> PRT

〈213〉 Homo sapiens

<400> 78

Met Lys Ser Leu Ile Leu Leu Ala Ile Leu Ala Ala Leu Ala Val Val

1 5 10 15

Thr Leu Cys Tyr Glu Ser His Glu Ser Met Glu Ser Tyr Glu Leu Asn

20 25 30

Pro Phe Ile Asn Arg Arg Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln

35 40 45

Arg Trp Arg Ala Lys Val Gln Glu Arg Ile Arg Glu Arg Ser Lys Pro

50

55

60

Val His Glu Leu Asn Arg Glu Ala Cys Asp Asp Tyr Arg Leu Cys Glu

65

70

75

80

Arg Tyr Ala Met Val Tyr Gly Tyr Asn Ala Ala Tyr Asn Arg Tyr Phe

85

90

95

Arg Lys Arg Arg Gly Thr Lys

100

<210> 79

<211> 1775

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (6).. (1148)

<400> 79

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Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val

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5

10

15

ttg gcc gag aac tcg gat gat tat gat ctc atg tat gtg aat ttg gac 98

Leu Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp

20

25

30

aac gaa ata gac aat gga ctc cat ccc act gag gac ccc acg ccg tgc 146

Asn Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys

35

40

45

gcc tgc ggt cag gag cac tcg gaa tgg gac aag ctc ttc atc atg ctg 194

Ala Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu
 50 55 60
 gag aac tcg cag atg aga gag cgc atg ctg ctg caa gcc acg gac gac 242
 Glu Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp
 65 70 75
 gtc ctg cgg ggc gag ctg cag agg ctg cgg gag gag ctg ggc cgg ctc 290
 Val Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu
 80 85 90 95
 gcg gaa agc ctg gcg agg ccg tgc gcg ccg ggg gct ccc gca gag gcc 338
 Ala Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala
 100 105 110
 agg ctg acc agt gct ctg gac gag ctg ctg cag gcg acc cgc gac gcg 386
 Arg Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala
 115 120 125
 ggc cgc agg ctg gcg cgt atg gag ggc gcg gag gcg cag cgc cca gag 434
 Gly Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu
 130 135 140
 gag gcg ggg cgc gcc ctg gcc gcg gtg cta gag gag ctg cgg cag acg 482
 Glu Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr
 145 150 155
 cga gcc gac ctg cac gcg gtg cag ggc tgg gct gcc cgg agc tgg ctg 530
 Arg Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu
 160 165 170 175
 ccg gca ggt tgt gaa aca gct att tta ttc cca atg cgt tcc aag aag 578
 Pro Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys
 180 185 190

att ttt gga agc gtg cat cca gtg aga cca atg agg ctt gag tct ttt 626
 Ile Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe
 195 200 205

agt gcc tgc att tgg gtc aaa gcc aca gat gla tta aac aaa acc atc 674
 Ser Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile
 210 215 220

ctg ttt tcc tat ggc aca aag agg aat cca lat gaa atc cag ctg tat 722
 Leu Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr
 225 230 235

ctc agc tac caa tcc ata gtg ttt gtg gtg ggt gga gag gag aac aaa 770
 Leu Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys
 240 245 250 255

ctg gtt gct gaa gcc atg gtt tcc ctg gga agg tgg acc cac ctg tgc 818
 Leu Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys
 260 265 270

ggc acc tgg aat tca gag gaa ggg ctc aca tcc ttg tgg gta aat ggt 866
 Gly Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly
 275 280 285

gaa ctg gcg gct acc act gtt gag atg gcc aca ggt cac att gtt cct 914
 Glu Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro
 290 295 300

gag gga gga atc ctg cag att ggc caa gaa aag aat ggc tgc tgt gtg 962
 Glu Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val
 305 310 315

ggt ggt ggc ttt gat gaa aca tta gcc ttc tct ggg aga ctc aca ggc 1010
 Gly Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly
 320 325 330 335

ttc aat atc tgg gat agt gtt ctt agc aat gaa gag ata aga gag acc 1058

Phe Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr

340

345

350

gga gga gca gag tct tgt cac atc cgg ggg aat att gtt ggg tgg gga 1106

Gly Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly

355

360

365

gtc aca gag atc cag cca cat gga gga gct cag tat gtt tca 1148

Val Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser

370

375

380

taaatgttgt gaaactccac ttgaagccaa agaaagaaac tcacacttaa aacacatgcc 1208

agttgggaag gtcgtaaaac tcagtgcata ataggaacac ttgagactaa tgaaagagag 1268

agttgagacc aatcttttatt tgtactggcc aaatactgaa taaacagttg aaggaaagac 1328

attggaaaaa gcttttgagg ataatgttac tagactttat gccatgggtgc tttcagttta 1388

atgctgtgtc tctgtcagat aaactctcaa ataattaaaa aggactgtat tgttgaacag 1448

agggacaatt gttttacttt tctttggta attttgtttt ggccagagat gaattttaca 1508

ttggaagaat aacaaaataa gatttgttgt ccattgttca ttgttatagg tatgtacctt 1568

attacaaaaa aaatgatgaa aacatattta tactacaagg tgacttaaca actataaatg 1628

tagtttatgt gttataatcg aatgtcacgt ttttgagaag atagtcatat aagtttatatt 1688

gcaaaaggga ttgtatttaa tllaagacta tttttgtaa gctctactgt aaataaaaata 1748

ttttataaaa ctaaaaaaaa aaaaaaa 1775

<210> 80

<211> 381

<212> PRT

<213> Homo sapiens

<400> 80

Met His Leu Leu Ala Ile Leu Phe Cys Ala Leu Trp Ser Ala Val Leu

1	5	10	15
Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp Asn			
20	25	30	
Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys Ala			
35	40	45	
Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu Glu			
50	55	60	
Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp Val			
65	70	75	80
Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu Ala			
85	90	95	
Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala Arg			
100	105	110	
Leu Thr Ser Ala Leu Asp Glu Leu Leu Gln Ala Thr Arg Asp Ala Gly			
115	120	125	
Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu Glu			
130	135	140	
Ala Gly Arg Ala Leu Ala Ala Val Leu Glu Glu Leu Arg Gln Thr Arg			
145	150	155	160
Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu Pro			
165	170	175	
Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys Ile			
180	185	190	
Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe Ser			
195	200	205	
Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile Leu			

210	215	220	
Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr Leu			
225	230	235	240
Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys Leu			
245	250	255	
Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys Gly			
260	265	270	
Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly Glu			
275	280	285	
Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro Glu			
290	295	300	
Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val Gly			
305	310	315	320
Gly Gly Phe Asp Glu Thr Leu Ala Phe Ser Gly Arg Leu Thr Gly Phe			
325	330	335	
Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr Gly			
340	345	350	
Gly Ala Glu Ser Cys His Ile Arg Gly Asn Ile Val Gly Trp Gly Val			
355	360	365	
Thr Glu Ile Gln Pro His Gly Gly Ala Gln Tyr Val Ser			
370	375	380	

<210> 81

<211> 2312

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (146).. (1192)

<400> 81

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 ccacctccga ccaccgccag cgctccaggc cccgcgtcc ccgctcgccg ccaccgcgcc 120
 ctccgctccg cccgcagtc caacc atg acc gcc gcc agt atg ggc ccc gtc 172

Met Thr Ala Ala Ser Met Gly Pro Val

1 5

cgc gtc gcc ttc gtg gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc 220

Arg Val Ala Phe Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val

10 15 20 25

ggc cag aac tgc agc ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg 268

Gly Gln Asn Cys Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro

30 35 40

cgc tgc ccg gcg ggc gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc 316

Arg Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys

45 50 55

cgc gtc tgc gcc aag cag ctg ggc gag ctg tgc acc gag cgc gac ccc 364

Arg Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro

60 65 70

tgc gac ccg cac aag ggc ctc ttc tgt gac ttc ggc tcc ccg gcc aac 412

Cys Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn

75 80 85

cgc aag atc ggc gtg tgc acc gcc aaa gat ggt gct ccc tgc atc ttc 460

Arg Lys Ile Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe

90 95 100 105

ggt ggt acg gtg tac cgc agc gga gag tcc ttc cag agc agc tgc aag 508

Gly Gly Thr Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys
 110 115 120
 tac cag tgc acg tgc ctg gac ggg gcg gtg ggc tgc atg ccc ctg tgc 556
 Tyr Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys
 125 130 135
 agc atg gac gtt cgt ctg ccc agc cct gac tgc ccc ttc ccg agg agg 604
 Ser Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg
 140 145 150
 gtc aag ctg ccc ggg aaa tgc tgc gag gag tgg gtg tgt gac gag ccc 652
 Val Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro
 155 160 165
 aag gac caa acc gtg gtt ggg cct gcc ctc gcg gct tac cga ctg gaa 700
 Lys Asp Gln Thr Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu
 170 175 180 185
 gac acg ttt ggc cca gac cca act atg att aga gcc aac tgc ctg gtc 748
 Asp Thr Phe Gly Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val
 190 195 200
 cag acc aca gag tgg agc gcc tgt tcc aag acc tgt ggg atg ggc atc 796
 Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile
 205 210 215
 tcc acc cgg gtt acc aat gac aac gcc tcc tgc agg cta gag aag cag 844
 Ser Thr Arg Val Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln
 220 225 230
 agc cgc ctg tgc atg gtc agg cct tgc gaa gct gac ctg gaa gag aac 892
 Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn
 235 240 245

att aag aag ggc aaa aag tgc atc cgt act ccc aaa atc tcc aag cct 940
 Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro
 250 255 260 265
 atc aag ttt gag ctt tct ggc tgc acc agc atg aag aca tac cga gct 988
 Ile Lys Phe Glu Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala
 270 275 280
 aaa ttc tgt gga gta tgt acc gac ggc cga tgc tgc acc ccc cac aga 1036
 Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg
 285 290 295
 acc acc acc ctg ccg gtg gag ttc aag tgc cct gac ggc gag gtc atg 1084
 Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met
 300 305 310
 aag aag aac atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt 1132
 Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys
 315 320 325
 ccc gga gac aat gac atc ttt gaa tgc ctg tac tac agg aag atg tac 1180
 Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr
 330 335 340 345
 gga gac atg gca tgaagccaga gaggagaga cattaactca ttagactgga 1232
 Gly Asp Met Ala
 acttgaactg attcacatct catttttccg taaaaatgat ttcagtagca caagttatit 1292
 aaatctgtit ttctaactgg gggaaaagat tcccacccaa ttcaaaacat tgtgccatgt 1352
 caaacaata gtctatcttc cccagacact ggtttgaaga atgttaagac ttgacagtgg 1412
 aactacatta gtacacagca ccagaatgta tattaaggig tggttttagg agcagtggga 1472
 gggtaccagc agaaaggta gtaacatcag atagctctta tacgagtaat atgcctgcta 1532
 tttgaagigt aattgagaag gaaaatttta ggtgtctcac tgacctgect gtagccccag 1592
 tgacagctag gatgtgcatt ctccagccat caagagactg agtcaagttg ttccttaagt 1652

cagaacagca gactcagctc tgacattctg attcgaatga cactgttcag gaatcggaat 1712
 cctgtcagatt agactggaca gcttgtggca agtgaatttc ctgtaacaag ccagatTTTT 1772
 taaaatttat attgtaaata ttgtgtgtgt gtgtgtgtgt gtatatatat atatatatgt 1832
 acagttaatct aagttaattt aaagtgtttt gtgccttttt atttttgttt ttaatgcttt 1892
 gatatttcaa tgttagcctc aatttctgaa caccataggt agaattgtaaa gcttgtctga 1952
 tcgttcaaag catgaaatgg atacattatat ggaaattctc tcagatagaa tgacagtccg 2012
 tcaaaacaga ttgtttgcaa aggggaggca tcagtgtcct tggcaggctg atttctaggt 2072
 aggaaatgtg gtagctcagc ctccacttta atgaacaaat ggccctttatt aaaaactgag 2132
 tgactctata tagctgatca gttttttcac ctggaagcat ttgtttctac ttgatataga 2192
 ctgtttttcg gacagtttat ttgttgagag tgtgacaaaa agttacatgt ttgcaccttt 2252
 ctagtgtaaa ataaagtata ttttttctaa aaaaaaaaaa aaacgacagc aacggaattc 2312

<210> 82

<211> 349

<212> PRT

<213> Homo sapiens

<400> 82

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu

1	5	10	15
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Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro

20	25	30
----	----	----

Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser

35	40	45
----	----	----

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu

50	55	60
----	----	----

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu

65	70	75	80
----	----	----	----

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr			
85	90	95	
Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser			
100	105	110	
Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp			
115	120	125	
Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro			
130	135	140	
Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys			
145	150	155	160
Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly			
165	170	175	
Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro			
180	185	190	
Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala			
195	200	205	
Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp			
210	215	220	
Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg			
225	230	235	240
Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys			
245	250	255	
Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly			
260	265	270	
Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr			
275	280	285	

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu

290

295

300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile

305

310

315

320

Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe

325

330

335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala

340

345

<210> 83

<211> 2954

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (173).. (1525)

<400> 83

gaattcccaa acglgcacag gggagtgagg gcagggcgct cgcagggggc acgcagggag 60

ggcccagggc gccagggagg ccgcgccggg ctaatccgaa ggggctgcga ggtcaggctg 120

taaccgggtc aatgtgtgga atatiggggg gctcggctgc agacttggcc aa atg gac 178

Met Asp

1

ggg act att aag gag gct ctg tcg glg glg agc gac gac cag tcc ctc 226

Gly Thr Ile Lys Glu Ala Leu Ser Val Val Ser Asp Asp Gln Ser Leu

5

10

15

ttt gac tca gcg tac gga gcg gca gcc cat ctc ccc aag gcc gac atg 274

Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala Asp Met

20	25	30	
act gcc tcg ggg agt cct gac tac ggg cag ccc cac aag atc aac ccc			322
Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile Asn Pro			
35	40	45	50
ctc cca cca cag cag gag tgg atc aat cag cca gtg agg gtc aac gtc			370
Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val Asn Val			
55	60	65	
aag cgg gag tat gac cac atg aat gga tcc agg gag tct ccg gtg gac			418
Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro Val Asp			
70	75	80	
tgc agc gtt agc aaa tgc agc aag ctg gtg ggc gga ggc gag tcc aac			466
Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu Ser Asn			
85	90	95	
ccc atg aac tac aac agc tat atg gac gag aag aat ggc ccc cct cct			514
Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro Pro Pro			
100	105	110	
ccc aac atg acc acc aac gag agg aga gtc atc gtc ccc gca gac ccc			562
Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala Asp Pro			
115	120	125	130
aca ctg tgg aca cag gag cat gtg agg caa tgg ctg gag tgg gcc ata			610
Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp Ala Ile			
135	140	145	
aag gag tac agc ttg atg gag atc gac aca tcc ttt ttc cag aac atg			658
Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln Asn Met			
150	155	160	
gat ggc aag gaa ctg tgt aaa atg aac aag gag gac ttc ctc cgc gcc			706
Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu Arg Ala			

165	170	175	
acc acc ctc tac aac acg gaa gtg ctg ttg tca cac ctc agt tac ctc	754		
Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser Tyr Leu			
180	185	190	
agg gaa agt tca ctg ctg gcc tat aat aca acc tcc cac acc gac caa	802		
Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr Asp Gln			
195	200	205	210
tcc tca cga ttg agt gtc aaa gaa gac cct tct tat gac tca gtc aga	850		
Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser Val Arg			
215	220	225	
aga gga gct tgg ggc aat aac atg aat tct ggc ctc aac aaa agt cct	898		
Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys Ser Pro			
230	235	240	
ccc ctt gga ggg gca caa acg atc agt aag aat aca gag caa cgg ccc	946		
Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln Arg Pro			
245	250	255	
cag cca gat ccg tat cag atc ctg ggc ccg acc agc agt cgc cta gcc	994		
Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg Leu Ala			
260	265	270	
aac cct gga agc ggg cag atc cag ctg tgg caa ttc ctc ctg gag ctg	1042		
Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu			
275	280	285	290
ctc tcc gac agc gcc aac gcc agc tgt atc acc tgg gag ggg acc aac	1090		
Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly Thr Asn			
295	300	305	
ggg gag ttc aaa atg acg gac ccc gat gag gtg gcc agg cgc tgg ggc	1138		

Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg Trp Gly
 310 315 320
 gag cgg aaa agc aag ccc aac atg aat tac gac aag ctg agc cgg gcc 1186
 Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala
 325 330 335
 ctc cgt tat tac tat gat aaa aac att atg acc aaa gtg cac ggc aaa 1234
 Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His Gly Lys
 340 345 350
 aga tat gct tac aaa ttt gac ttc cac ggc att gcc cag gct ctg cag 1282
 Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala Leu Gln
 355 360 365 370
 cca cat ccg acc gag tcg tcc atg tac aag tac cct tct gac atc tcc 1330
 Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp Ile Ser
 375 380 385
 tac atg cct tcc caa cat gcc cac cag cag aag gtg aac ttt gtc cct 1378
 Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe Val Pro
 390 395 400
 ccc cat cca tcc tcc atg cct gtc act tcc tcc agc ttc ttt gga gcc 1426
 Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe Gly Ala
 405 410 415
 gca tca caa tac tgg acc tcc acg ggg gga atc tac ccc aac ccc aac 1474
 Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn Pro Asn
 420 425 430
 gtc ccc cgc cat cct aac acc cac gtg cct tca cac tta ggc agc tac 1522
 Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly Ser Tyr
 435 440 445 450
 tac tagaagctta ctcatcagtg gccttctagc tgaagcccat cctgcacact 1575

Tyr

tactggatgc ttggactca acaggacata tgggacctg aagggaagac aaaactggat 1635
gttctttctt gttggataga acctttgat ttgttcttta aaaatatatt ttttaatgtt 1695
ggtaactttt gcttccctca ccgaacaaa gagatgaata attccatggg ccagtatgcc 1755
agtttgaatt ctacgtctcc tagcatcttg tgagttgcat attaagatta ctggaatggt 1815
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tttcttgtca atacacgggg ttacgtatga cacagaalca tggacttaac ccgtcatgtt 1935
ctggtttgag atttagtgac aaatagaggt gggaagctta taatctaatt ttaggaggac 1995
caaattcagc ggaatggcaac tggaacattg attgtaagc cagtgaagtt ttacaccaac 2055
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ctcagttgac agtatgcact cagctgacca ctctctctag aaatagtcac gatatgaact 2175
aagaaatttt aatgcaata catacattcc tgaagacgg ggaattaaat tactaatttt 2235
ttttttttaa atgatgacag tggcccaga acttgaaaaa gttgtaggga ttcttaact 2295
caagcagatt cgcaagtgt gtgcgttgt cagaccatca gaccagggcc aaccaatcag 2355
aaggcaactt actgtataaa ttatgcagag ttattttcct atatctcaca gtaaaaaa 2415
ataaataatt aaaaattaag aataaataaa cgagttgacc tcggtcaca aagcagtttt 2475
actatcgaat caatcgtgt tatTTTTTTT taatgtaatt tglacatctt ttccaatct 2535
gtacatttgg gctgtcttgt atgtttttat gctccttttt aaaaagcata atatgcctat 2595
agctgaaaag gaaacagggc tgtttaagtc actgacttat gagaaagcaa agcactggta 2655
cagttattta acaggcatc acaagcaggg aaaagataat ccatttagat ctttaatgct 2715
ttggaaatgc gtttaacagt actgcaataa tcacagctct gggaaaaaca acgaaacttt 2775
cccttgttga gaggagggt ttctctgtc tatataagca acatattttt agacattaaa 2835
atatatataa ttttgcaggt aattgttgac ttttttaact atattaagt ttaagctgac 2895
aactgtcaaa gaagaccatg ttgtaaaata atttgactaa ataaatgggt ccttctctc 2954

<210> 84

<211> 451

<212> PRT

<213> Homo sapiens

<400> 84

Met Asp Gly Thr Ile Lys Glu Ala Leu Ser Val Val Ser Asp Asp Gln

1 5 10 15

Ser Leu Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala

20 25 30

Asp Met Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile

35 40 45

Asn Pro Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val

50 55 60

Asn Val Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro

65 70 75 80

Val Asp Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu

85 90 95

Ser Asn Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro

100 105 110

Pro Pro Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala

115 120 125

Asp Pro Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp

130 135 140

Ala Ile Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln

145 150 155 160

Asn Met Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu

165 170 175

Arg Ala Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser

180	185	190	
Tyr Leu Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr			
195	200	205	
Asp Gln Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser			
210	215	220	
Val Arg Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys			
225	230	235	240
Ser Pro Pro Leu Gly Gly Ala Gln Thr Ile Ser Lys Asn Thr Glu Gln			
245	250	255	
Arg Pro Gln Pro Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg			
260	265	270	
Leu Ala Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu			
275	280	285	
Glu Leu Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly			
290	295	300	
Thr Asn Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg			
305	310	315	320
Trp Gly Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser			
325	330	335	
Arg Ala Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His			
340	345	350	
Gly Lys Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala			
355	360	365	
Leu Gln Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp			
370	375	380	
Ile Ser Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe			
385	390	395	400

Val Pro Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe

405

410

415

Gly Ala Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn

420

425

430

Pro Asn Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly

435

440

445

Ser Tyr Tyr

450

<210> 85

<211> 1817

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (361)

<400> 85

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Gln Gln Asp Gly Glu Gly His Thr Gln Asp Thr Glu Leu Val Glu Thr

1

5

10

15

agg cct gca ggg gat gga acc ttc cag aag tgg gca gct gtg gtg gtg 97

Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val

20

25

30

cct tct gga gag gag cag aga tac acg tgc cat gtg cag cat gag ggg 145

Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly

35

40

45

cta ccc gag ccc gtc acc ctg aga tgg aag ccg gct tcc cag ccc acc 193

Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala Ser Gln Pro Thr
 50 55 60
 atc ccc atc gtg ggc atc att gct ggc ctg gtt ctc ctt gga tct gtg 241
 Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val
 65 70 75 80
 gtc tct gga gct gig gtt gct gct gig ata tgg agg aag aag agc tca 289
 Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser
 85 90 95
 ggt gga aaa gga ggg agc tac tct aag gct gag tgg agc gac agl gcc 337
 Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala
 100 105 110
 cag ggg tct gag tct cac agc tgg taaagcciga gacagctgcc ttgtgtgcga 391
 Gln Gly Ser Glu Ser His Ser Leu
 115 120
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 aaactttgaa glaaaataaa agctgtgttt gagcatcaaa aaaaaa 1817

<210> 86

<211> 120

<212> PRT

<213> Homo sapiens

<400> 86

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Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val

20 25 30

Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly

35 40 45

Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala Ser Gln Pro Thr

50 55 60

Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val

65 70 75 80
 Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser
 85 90 95
 Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala
 100 105 110
 Gln Gly Ser Glu Ser His Ser Leu
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<210> 87

<211> 2876

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1281)

<400> 87

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 tctgagaact tcagg atg cag atg tct cca gcc ctc acc tgc cta gtc ctg 111

Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu

1 5 10

ggc ctg gcc ctt gtc ttt ggt gaa ggg tct gct gtg cac cat ccc cca 159

Gly Leu Ala Leu Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro

15 20 25

tcc tac gtg gcc cac ctg gcc tca gac ttc ggg gtg agg gtg ttt cag 207

Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln

30 35 40

cag gtg gcg cag gcc tcc aag gac cgc aac gtg gtt ttc tca ccc tat 255

Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr
 45 50 55 60
 ggg gtg gcc tgc gtg ttg gcc atg ctc cag ctg aca aca gga gga gaa 303
 Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu
 65 70 75
 acc cag cag cag att caa gca gct atg gga ttc aag att gat gac aag 351
 Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys
 80 85 90
 ggc atg gcc ccc gcc ctc cgg cat ctg tac aag gag ctc atg ggg cca 399
 Gly Met Ala Pro Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro
 95 100 105
 tgg aac aag gat gag atc agc acc aca gac gcg atc ttc gtc cag cgg 447
 Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg
 110 115 120
 gat ctg aag ctg gtc cag ggc ttc atg ccc cac ttc ttc agg ctg ttc 495
 Asp Leu Lys Leu Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe
 125 130 135 140
 cgg agc acg gtc aag caa glg gac ttt tca gag gtg gag aga gcc aga 543
 Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg
 145 150 155
 ttc atc atc aat gac tgg gtg aag aca cac aca aaa ggt atg atc agc 591
 Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser
 160 165 170
 aac ttg ctt ggg aaa gga gcc gtg gac cag ctg aca cgg ctg gtg ctg 639
 Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu
 175 180 185
 glg aat gcc ctc tac ttc aac ggc cag tgg aag act ccc ttc ccc gac 687

Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp
 190 195 200
 tcc agc acc cac cgc cgc ctc ttc cac aaa tca gac ggc agc act gtc 735
 Ser Ser Thr His Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val
 205 210 215 220
 tct gtg ccc atg atg gct cag acc aac aag ttc aac tat act gag ttc 783
 Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe
 225 230 235
 acc acg ccc gat ggc cat tac tac gac atc ctg gaa ctg ccc tac cac 831
 Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His
 240 245 250
 ggg gac acc ctc agc atg ttc att get gcc cct tat gaa aaa gag gtg 879
 Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val
 255 260 265
 cct ctc tct gcc ctc acc aac att ctg agt gcc cag ctc atc agc cac 927
 Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His
 270 275 280
 tgg aaa ggc aac atg acc agg ctg ccc cgc ctc ctg gtt ctg ccc aag 975
 Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys
 285 290 295 300
 ttc tcc ctg gag act gaa gtc gac ctc agg aag ccc cta gag aac ctg 1023
 Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu
 305 310 315
 gga atg acc gac atg ttc aga cag ttt cag gct gac ttc acg agt ctt 1071
 Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu
 320 325 330

tca gac caa gag cct ctc cac gtc gcg cag gcg ctg cag aaa gtg aag 1119
 Ser Asp Gln Glu Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys
 335 340 345
 atc gag gtg aac gag agt ggc acg gtg gcc tcc tca tcc aca gct gtc 1167
 Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val
 350 355 360
 ata gtc tca gcc cgc atg gcc ccc gag gag atc atc atg gac aga ccc 1215
 Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro
 365 370 375 380
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 Phe Leu Phe Val Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met
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 Gly Gln Val Met Glu Pro
 400
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 gaagc 2876

<210> 88

<211> 402

<212> PRT

<213> Homo sapiens

<400> 88

Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu

Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro Ser Tyr Val Ala

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5

10

15

His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln

20

25

30

Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser

35	40	45	
Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln			
50	55	60	
Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro			
65	70	75	80
Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp			
85	90	95	
Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu			
100	105	110	
Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val			
115	120	125	
Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn			
130	135	140	
Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly			
145	150	155	160
Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu			
165	170	175	
Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His			
180	185	190	
Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met			
195	200	205	
Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp			
210	215	220	
Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu			
225	230	235	240
Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala			

245	250	255	
Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His Trp Lys Gly Asn			
260	265	270	
Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys Phe Ser Leu Glu			
275	280	285	
Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu Gly Met Thr Asp			
290	295	300	
Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu			
305	310	315	320
Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn			
325	330	335	
Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala			
340	345	350	
Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val			
355	360	365	
Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met Gly Gln Val Met			
370	375	380	
Glu Pro			
385			

<210> 89

<211> 1412

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (52).. (1341)

<400> 89

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Met Ser

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ttc acc act cgc tcc acc ttc tcc acc aac tac cgg tcc ctg ggc tct 105

Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu Gly Ser

5

10

15

gtc cag gcg ccc agc tac ggc gcc cgg ccg gtc agc agc gcg gcc agc 153

Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala Ala Ser

20

25

30

gtc tat gca ggc gct ggg ggc tct ggt tcc cgg atc tcc gtg tcc cgc 201

Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val Ser Arg

35

40

45

50

tcc acc agc ttc agg ggc ggc atg ggg tcc ggg ggc ctg gcc acc ggg 249

Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr Gly

55

60

65

ata gcc ggg ggt ctg gca gga atg gga ggc atc cag aac gag aag gag 297

Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys Glu

70

75

80

acc atg caa agc ctg aac gac cgc ctg gcc tct tac ctg gac aga gtg 345

Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg Val

85

90

95

agg agc ctg gag acc gag aac cgg agg ctg gag agc aaa atc cgg gag 393

Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg Glu

100

105

110

cac ttg gag aag aag gga ccc cag gtc aga gac tgg agc cat tac ttc 441

His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr Phe

115	120	125	130	
aag atc atc gag gac ctg agg gct cag atc ttc gca aat act gtg gac	489			
Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val Asp				
135	140	145		
aat gcc cgc atc gtt ctg cag att gac aat gcc cgt ctt gct gct gat	537			
Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala Asp				
150	155	160		
gac ttt aga gtc aag tat gag aca gag ctg gcc atg cgc cag tct gtg	585			
Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln Ser Val				
165	170	175		
gag aac gac atc cat ggg ctc cgc aag gtc att gat gac acc aat atc	633			
Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn Ile				
180	185	190		
aca cga ctg cag ctg gag aca gag atc gag gct ctc aag gag gag ctg	681			
Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu Leu				
195	200	205	210	
ctc ttc atg aag aag aac cac gaa gag gaa gta aaa ggc cta caa gcc	729			
Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln Ala				
215	220	225		
cag att gcc agc tct ggg ttg acc gtg gag gta gat gcc ccc aaa tct	777			
Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys Ser				
230	235	240		
cag gac ctc gcc aag atc atg gca gac atc cgg gcc caa tat gac gag	825			
Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp Glu				
245	250	255		
ctg gct cgg aag aac cga gag gag cta gac aag tac tgg tct cag cag	873			

Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln Gln
 260 265 270
 att gag gag agc acc aca gtg gtc acc aca cag tct gct gag gtt gga 921
 Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val Gly
 275 280 285 290
 gct gct gag acg acg ctc aca gag ctg aga cgt aca gtc cag tcc ttg 969
 Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser Leu
 295 300 305
 gag atc gac ctg gac tcc atg aga aat ctg aag gcc agc ttg gag aac 1017
 Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu Asn
 310 315 320
 agc ctg agg gag gtg gag gcc cgc tac gcc cta cag atg gag cag ctc 1065
 Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln Leu
 325 330 335
 aac ggg atc ctg ctg cac ctt gag tca gag ctg gca cag acc cgg gca 1113
 Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg Ala
 340 345 350
 gag gga cag cgc cag gcc cag gag tat gag gcc ctg ctg aac atc aag 1161
 Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile Lys
 355 360 365 370
 gtc aag ctg gag gct gag atc gcc acc tac cgc cgc ctg ctg gaa gat 1209
 Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Asp
 375 380 385
 ggc gag gac ttt aat ctt ggt gat gcc ttg gac agc agc aac tcc atg 1257
 Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser Met
 390 395 400
 caa acc atc caa aag acc acc acc cgc cgg ata gtg gat ggc aaa gtg 1305

Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly Lys Val

405

410

415

gtg tct gag acc aat gac acc aaa gtt ctg agg cat taagccagca 1351

Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His

420

425

430

gaagcagggt accctttggg gagcaggagg ccaataaaaa gttcagagtt cattggaigt 1411

c 1412

<210> 90

<211> 430

<212> PRT

<213> Homo sapiens

<400> 90

Met Ser Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu

1

5

10

15

Gly Ser Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala

20

25

30

Ala Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val

35

40

45

Ser Arg Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala

50

55

60

Thr Gly Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu

65

70

75

80

Lys Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp

85

90

95

Arg Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile

100

105

110

Arg Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His
 115 120 125
 Tyr Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr
 130 135 140
 Val Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala
 145 150 155 160
 Ala Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln
 165 170 175
 Ser Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr
 180 185 190
 Asn Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu
 195 200 205
 Glu Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu
 210 215 220
 Gln Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro
 225 230 235 240
 Lys Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr
 245 250 255
 Asp Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser
 260 265 270
 Gln Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu
 275 280 285
 Val Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln
 290 295 300
 Ser Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu
 305 310 315 320

Glu Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu

325

330

335

Gln Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr

340

345

350

Arg Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn

355

360

365

Ile Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu

370

375

380

Glu Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn

385

390

395

400

Ser Met Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly

405

410

415

Lys Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His

420

425

430

<210> 91

<211> 1040

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (171).. (968)

<400> 91

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ggtgcctgaa tgggaacccc ccgaagcgcc tgaaaaggag agacaggagg atg atg 176

Met Met

1

tcc cag ctg gag ctg ctg agt ggg gga gag atg ctg tgc ggt ggc ttc 224
 Ser Gln Leu Glu Leu Leu Ser Gly Gly Glu Met Leu Cys Gly Gly Phe
 5 10 15
 tac cct cgg ctg tcc tgc tgc ctg cgg agt gac agc ccg ggg cta ggg 272
 Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly Leu Gly
 20 25 30
 cgc ctg gag aat aag ata ttt tct gtt acc aac aac aca gaa tgt ggg 320
 Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu Cys Gly
 35 40 45 50
 aag tta ctg gag gaa atc aaa tgt gca ctt tgc tct cca cat tct caa 368
 Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His Ser Gln
 55 60 65
 agc ctg ttc cac tca cct gag aga gaa gtc ttg gaa aga gac cta gta 416
 Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp Leu Val
 70 75 80
 ctt cct ctg ctg tgc aaa gac tat tgc aaa gaa ttc ttt tac act tgc 464
 Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr Thr Cys
 85 90 95
 cga ggc cat att cca ggt ttc ctt caa aca act gcg gat gag ttt tgc 512
 Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu Phe Cys
 100 105 110
 ttt tac tat gca aga aaa gat ggt ggg ttg tgc ttt cca gat ttt cca 560
 Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp Phe Pro
 115 120 125 130
 aga aaa caa gtc aga gga cca gca tct aac tac ttg gac cag atg gaa 608
 Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln Met Glu

135	140	145	
gaa tat gac aaa gtg gaa gag atc agc aga aag cac aaa cac aac tgc			656
Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His Asn Cys			
150	155	160	
ttc tgt att cag gag gtt gtg agt ggg ctg cgg cag ccc gtt ggt gcc			704
Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val Gly Ala			
165	170	175	
ctg cat agt ggg gat ggc tcg caa cgt ctc ttc att ctg gaa aaa gaa			752
Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu Lys Glu			
180	185	190	
ggt tat gtg aag ata ctt acc cct gaa gga gaa att ttc aag gag cct			800
Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys Glu Pro			
195	200	205	210
tat ttg gac att cac aaa ctt gtt caa agt gga ata aag gtt ggc ttt			848
Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val Gly Phe			
215	220	225	
tta aat ttt att tat ttt tgt gct ggc tac gtt aat ttt att tta gtg			896
Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile Leu Val			
230	235	240	
tta cct tcc tca ctg aag gta ttt ctt tgt aat aaa aga aag aat ctt			944
Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys Asn Leu			
245	250	255	
gca gga gaa aat aag ggg gca aca taagaacaa laattatggc accigaatta			998
Ala Gly Glu Asn Lys Gly Ala Thr			
260	265		
ggacagtgac attaaakggt ggctktttaw attttaaaaa aa			1040

<210> 92

<211> 266

<212> PRT

<213> Homo sapiens

<400> 92

Met Met Ser Gln Leu Glu Leu Leu Ser Gly Gly Glu Met Leu Cys Gly
 1 5 10 15
 Gly Phe Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly
 20 25 30
 Leu Gly Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu
 35 40 45
 Cys Gly Lys Leu Leu Glu Glu Ile Lys Cys Ala Leu Cys Ser Pro His
 50 55 60
 Ser Gln Ser Leu Phe His Ser Pro Glu Arg Glu Val Leu Glu Arg Asp
 65 70 75 80
 Leu Val Leu Pro Leu Leu Cys Lys Asp Tyr Cys Lys Glu Phe Phe Tyr
 85 90 95
 Thr Cys Arg Gly His Ile Pro Gly Phe Leu Gln Thr Thr Ala Asp Glu
 100 105 110
 Phe Cys Phe Tyr Tyr Ala Arg Lys Asp Gly Gly Leu Cys Phe Pro Asp
 115 120 125
 Phe Pro Arg Lys Gln Val Arg Gly Pro Ala Ser Asn Tyr Leu Asp Gln
 130 135 140
 Met Glu Glu Tyr Asp Lys Val Glu Glu Ile Ser Arg Lys His Lys His
 145 150 155 160
 Asn Cys Phe Cys Ile Gln Glu Val Val Ser Gly Leu Arg Gln Pro Val

165	170	175	
Gly Ala Leu His Ser Gly Asp Gly Ser Gln Arg Leu Phe Ile Leu Glu			
180	185	190	
Lys Glu Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys			
195	200	205	
Glu Pro Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val			
210	215	220	
Gly Phe Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile			
225	230	235	240
Leu Val Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys			
245	250	255	
Asn Leu Ala Gly Glu Asn Lys Gly Ala Thr			
260	265		

<210> 93

<211> 1639

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75).. (371)

<400> 93

agcagagcac acaagcttct aggacaagag ccaggaagaa accaccggaa ggaaccatct 60

cactgtgtgt aaac atg act tcc aag ctg gcc gtg gct ctc ttg gca gcc 110

Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala

1 5 10

ttc ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt 158

Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser

15

20

25

gct aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc 206

Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe

30

35

40

cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac 254

His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His

45

50

55

60

tgc gcc aac aca gaa att att gta aag ctt tct gat gga aga gag etc 302

Cys Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu

65

70

75

tgt ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt 350

Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe

80

85

90

ttg aag agg gct gag aat tca taaaaaaatt cattctctgt ggtatccaag 401

Leu Lys Arg Ala Glu Asn Ser

95

aatcagtgaa gatgccagtg aaacttcaag caaatctact tcaacacttc atgtattgtg 461

tgggtctgtt gtagggttgc cagatgcaat acaagattcc tggttaaatt tgaatttcag 521

taaacaatga atagtitttc attglacat gaaatacca gaacatactt atatglaaag 581

tattatttat ttgaatctac aaaaaacaac aaataatttt taaatataag gattttccta 641

gatattgcac gggagaatat acaaatagca aaattgagcc aaggccaag agaatatccg 701

aactttaatt tcaggaattg aatgggtttg ctagaatgig atatitgaag catcacataa 761

aaatgatggg acaataaatt ttgccataaa gtcaaattta gctggaaatc ctggattttt 821

ttctgttaaa tctggcaacc ctagtctgct agccaggatc cacaagtcct tgttccactg 881

tgccttgggt tctcctttat ttctaagtgg aaaaagtatt agccaccatc ttacctcaca 941

gtgatgttgt gaggacatgt ggaagcactt taagtttttt catcataaca taaattattt 1001

tcaagtgtaa cttattaacc tatttattat ttatgtatit atttaagcat caaatatttg 1061
 tgcaagaatt tggaaaaata gaagatgaat cattgattga atagttataa agatgttata 1121
 gtaaatllat tttatttttag atattaaatg atgttttatt agataaatit caatcaggg 1181
 ttttagatta aacaaagaaa caattgggia cccagttaaa ttttcatttc agataaacia 1241
 caaataatit tttagtataa gtacattatt gtttatctga aagttttaat tgaactaaca 1301
 atcctagttt gatactccca gicctgtcat tgccagctgt gttagtagtg ctgtgttgaa 1361
 ttacggaata atgagttaga actattaaaa cagccaaaac tccacagica atattagtaa 1421
 tttcttgctg gttgaaactt gtttattatg taaaaataga ttcttataat attattitaa 1481
 tgactgcatt ttlaaataca aggcattata tttttaactt taagatgtit ttatgtgctc 1541
 tccaaatitit ttttactgtt tctgatigta tggaaatata aaagtaaata tgaacattit 1601
 aaaatataat ttgttgtcaa agtaaaaaaa aaaaaaaa 1639

<210> 94

<211> 99

<212> PRT

<213> Homo sapiens

<400> 94

Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser

Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu

1

5

10

15

Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe

20

25

30

Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr

35

40

45

Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro

50

55

60

Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala

65 70 75 80

Glu Asn Ser

<210> 95

<211> 3293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (8).. (1945)

<400> 95

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Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Leu Ala Ala

1 5 10

tgc tgc tgc tgt cct cgc gtc gcg ggt gtg ccc gga gag gct gag cag 97

Cys Cys Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln

15 20 25 30

cct gcg cct gag ctg gtg gag gtg gaa gtg ggc agc aca gcc ctt ctg 145

Pro Ala Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu

35 40 45

aag tgc ggc ctc tcc cag tcc caa ggc aac ctc agc cat gtc gac tgg 193

Lys Cys Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp

50 55 60

ttt tct gtc cac aag gag aag cgg acg ctc atc ttc cgt gtg cgc cag 241

Phe Ser Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln

65 70 75

ggc cag ggc cag agc gaa cct ggg gag tac gag cag cgg ctc agc ctc 289

Gly Gln Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu
 80 85 90
 cag gac aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac 337
 Gln Asp Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp
 95 100 105 110
 gag cgc atc ttc ttg tgc cag ggc aag cgc cct cgg tcc cag gag tac 385
 Glu Arg Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr
 115 120 125
 cgc atc cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag 433
 Arg Ile Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln
 130 135 140
 gtc aac ccc ctg ggc atc cct gtg aac agt aag gag cct gag gag gtc 481
 Val Asn Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val
 145 150 155
 gct acc tgt gla ggg agg aac ggg tac ccc att cct caa gtc atc tgg 529
 Ala Thr Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp
 160 165 170
 tac aag aat ggc cgg cct ctg aag gag gag aag aac cgg gtc cac att 577
 Tyr Lys Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile
 175 180 185 190
 cag tgc tcc cag act gtg gag tgc agt ggt ttg tac acc ttg cag agt 625
 Gln Ser Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser
 195 200 205
 att ctg aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac 673
 Ile Leu Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr
 210 215 220

tgt gag ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc 721
 Cys Glu Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser
 225 230 235
 agg gaa gtc acc gtc cct gtt ttc tac cgg aca gaa aaa gtg tgg ctg 769
 Arg Glu Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu
 240 245 250
 gaa gtg gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc 817
 Glu Val Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile
 255 260 265 270
 agg tgt ttg gct gat ggc aac cct cca cca cac ttc agc atc agc aag 865
 Arg Cys Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys
 275 280 285
 cag aac ccc agc acc agg gag gca gag gaa gag aca acc aac gac aac 913
 Gln Asn Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn
 290 295 300
 ggg gtc ctg gtg ctg gag cct gcc cgg aag gaa cac agt ggg cgc tat 961
 Gly Val Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr
 305 310 315
 gaa tgt cag gcc tgg aac ttg gac acc atg ata tgc ctg ctg agt gaa 1009
 Glu Cys Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu
 320 325 330
 cca cag gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc 1057
 Pro Gln Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro
 335 340 345 350
 gca gcc cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag 1105
 Ala Ala Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu
 355 360 365

gca gag agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca 1153
 Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr
 370 375 380
 gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa 1201
 Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys
 385 390 395
 cgg gag gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata 1249
 Arg Glu Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile
 400 405 410
 ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc 1297
 Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro
 415 420 425 430
 cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg 1345
 Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met
 435 440 445
 gtg ttg aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc 1393
 Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile
 450 455 460
 tcc tgg aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag 1441
 Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln
 465 470 475
 cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag 1489
 Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu
 480 485 490
 aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc 1537
 Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser

495	500	505	510	
atc ctc ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc				1585
Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser				
	515	520	525	
aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga				1633
Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg				
	530	535	540	
gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg				1681
Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg				
	545	550	555	
ggc gtg gtc atc glg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg				1729
Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val				
	560	565	570	
ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc				1777
Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys				
575	580	585	590	
agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc				1825
Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr				
	595	600	605	
gaa ctt gla gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc				1873
Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly				
	610	615	620	
ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga				1921
Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly				
	625	630	635	
gag aaa tac atc gat ctg agg cat tagcccccga tcaacttcagc tcccttcct				1975
Glu Lys Tyr Ile Asp Leu Arg His				

640

645

gcctggacca ttcccagctc cctgcctact cttctctcag ccaaagctca aagggactag 2035
 agagaagcct cctgcctccc tgcctgcac acccccttc agagggccac tgggttagga 2095
 cctgaggacc tcacttggcc ctgcaaggcc cgttttcag ggaccagtcc accaccatct 2155
 cctccacgtt gagtgaagct cateccaagc aaggagcccc agtctccga ggggttagga 2215
 gagttcttg cagaacgtgt ttttcttta cacacattat gctgtaaata cgtcgtcct 2275
 gccagcagct gagctgggta gcctctctga gctggttcc tgcctcaaag gctggcattc 2335
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 aagtgcgtg ttacacccg ctccggagag caccacagca gcatccagaa gcagctgcag 2455
 tgcaagcttg catgcctgcg tgttgcctga ccacctcct gtctgcctct tcaaagctc 2515
 ctgtgacatt tttcttttg tcagaggcca ggaactgtgt cattcctta agatacgtc 2575
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 cacaaagta gacgagacca tcttgctaa caggcgaaa cctgtctct actaaaaata 2695
 caaaaaaaaa ttagctaggg gtagtggtg gcacctatag tccagctac tcggaaggct 2755
 gaagcaggag aatggatga atccaggagg tggagcttg agtagccga gaccgtgcca 2815
 ctgcactcca gccctggcaa cacagcgaga ctccgtctg agggaaaaa aaatcgtgt 2875
 cgtagcagct ggctctgtt cgagtcaggt gaattagcct caatccccgt gttcacttg 2935
 tcccatagcc ctcttgatgg atcacgtaa actgaaaggc agcggggagc agacaaagat 2995
 gaggtctaca ctgcttca tggggattaa agctatggtt atattagcac caacttcta 3055
 caaaccaagc tcaggacca accctagaag ggcctaatg agagaatgtt acttaggat 3115
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 gtgtgtatat atggtttgt caggltgtt aattgcaa tigtctctt tatatatgta 3235
 tgtatatata tatatgaaa tatatatata tatgaaaat aaagctta tgtccag 3293

<210> 96

<211> 646

<212> PRT

<213> Homo sapiens

<400> 96

Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Leu Ala Ala Cys Cys

1 5 10 15

Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala

20 25 30

Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys

35 40 45

Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser

50 55 60

Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln

65 70 75 80

Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp

85 90 95

Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg

100 105 110

Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile

115 120 125

Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn

130 135 140

Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr

145 150 155 160

Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys

165 170 175

Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser

180 185 190

Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
 195 200 205
 Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
 210 215 220
 Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
 225 230 235 240
 Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
 245 250 255
 Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
 260 265 270
 Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn
 275 280 285
 Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val
 290 295 300
 Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys
 305 310 315 320
 Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln
 325 330 335
 Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
 340 345 350
 Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
 355 360 365
 Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln
 370 375 380
 Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu
 385 390 395 400
 Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly

405	410	415	
Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp			
420	425	430	
Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu			
435	440	445	
Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp			
450	455	460	
Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val			
465	470	475	480
Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly			
485	490	495	
Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu			
500	505	510	
Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr			
515	520	525	
Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn			
530	535	540	
Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val			
545	550	555	560
Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly			
565	570	575	
Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg			
580	585	590	
Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu			
595	600	605	
Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu			

610 615 620
 Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys

625 630 635 640

Tyr Ile Asp Leu Arg His

645

<210> 97

<211> 1642

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (158).. (1279)

<400> 97

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 ggggaccagc agctgtcgcc gccgctctca gggigaagag ggaacagaaa tctttgcccc 120
 ctgactttgg aaatctcgtt taaccttcaa actggcg atg tca agg gtt cca agt 175

Met Ser Arg Val Pro Ser

1

5

cct cca cct ccg gca gaa atg teg agt ggc ccc gta gct gag agt tgg 223

Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp

10

15

20

tgc tac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc 271

Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile

25

30

35

aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt 319

Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser

40	45	50	
tct aca ttt tca tca gga gca aat gat aaa ctg aaa tgg tgt ttg cga	367		
Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg			
55	60	65	70
gta aac ccc aaa ggg tta gat gaa gaa agc aaa gat tac ctg tca ctt	415		
Val Asn Pro Lys Gly Leu Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu			
75	80	85	
tac ctg tta ctg gtc agc tgt cca aag agt gaa gtt cgg gca aaa ttc	463		
Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser Glu Val Arg Ala Lys Phe			
90	95	100	
aaa ttc tcc atc ctg aat gcc aag gga gaa gaa acc aaa gct atg gag	511		
Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu			
105	110	115	
agt caa cgg gca tat agg ttt gtg caa ggc aaa gac tgg gga ttc aag	559		
Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly Lys Asp Trp Gly Phe Lys			
120	125	130	
aaa ttc atc cgt aga gat ttt ctt ttg gat gag gcc aac ggg ctt ctc	607		
Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu			
135	140	145	150
cct gat gac aag ctt acc ctc ttc tgc gag gtg agt gtt gtg caa gat	655		
Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu Val Ser Val Val Gln Asp			
155	160	165	
tct gtc aac att tct ggc cag aat acc atg aac atg gta aag gtt cct	703		
Ser Val Asn Ile Ser Gly Gln Asn Thr Met Asn Met Val Lys Val Pro			
170	175	180	
gag tgc cgg ctg gca gat gag tta gga gga ctg tgg gag aat tcc cgg	751		
Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly Leu Trp Glu Asn Ser Arg			

185	190	195	
ttc aca gac tgc tgc ttg tgt gtt gcc ggc cag gaa ttc cag gct cac			799
Phe Thr Asp Cys Cys Leu Cys Val Ala Gly Gln Glu Phe Gln Ala His			
200	205	210	
aag gct atc tta gca gct cgt tct ccg gtt ttt agt gcc atg ttt gaa			847
Lys Ala Ile Leu Ala Ala Arg Ser Pro Val Phe Ser Ala Met Phe Glu			
215	220	225	230
cat gaa atg gag gag agc aaa aag aat cga gtt gaa atc aat gat gtg			895
His Glu Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Val			
235	240	245	
gag cct gaa gtt ttt aag gaa atg atg tgc ttc att tac acg ggg aag			943
Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys			
250	255	260	
gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac			991
Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Ala Asp			
265	270	275	
aag tat gcc ctg gag cgc tta aag gtc atg tgt gag gat gcc ctc tgc			1039
Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys			
280	285	290	
agt aac ctg tcc gtg gag aac gct gca gaa att ctc atc ctg gcc gac			1087
Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp			
295	300	305	310
ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac			1135
Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn			
315	320	325	
tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg			1183

Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val

330

335

340

gtg tca cat ccc cac ttg gtg gct gag gca tac cgc tct ctg gct tca 1231

Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser

345

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Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg Lys Arg Leu Lys Gln Ser

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Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met

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Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys
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 Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu
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 Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly
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 Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
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 Asn Met Val Lys Val Pro Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly
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 Leu Trp Glu Asn Ser Arg Phe Thr Asp Cys Cys Leu Cys Val Ala Gly
 195 200 205
 Gln Glu Phe Gln Ala His Lys Ala Ile Leu Ala Ala Arg Ser Pro Val
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 Phe Ser Ala Met Phe Glu His Glu Met Glu Glu Ser Lys Lys Asn Arg
 225 230 235 240
 Val Glu Ile Asn Asp Val Glu Pro Glu Val Phe Lys Glu Met Met Cys
 245 250 255
 Phe Ile Tyr Thr Gly Lys Ala Pro Asn Leu Asp Lys Met Ala Asp Asp

260 265 270
 Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met
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 Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln
 305 310 315 320
 Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser
 325 330 335
 Gly Trp Lys Ser Met Val Val Ser His Pro His Leu Val Ala Glu Ala
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Met Gly

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 Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys Gly Thr
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 Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp Ile Phe
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 Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu Val Lys
 35 40 45 50
 ggc ccc gac cct tcc agc cca gct ttc cgc atc gag gat gcc aac ctg 309
 Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala Asn Leu
 55 60 65
 atc ccc cct gtg cct gat gac aag ttc caa gac ctg gtg gat gct gtg 357
 Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp Ala Val
 70 75 80
 cgg gca gaa aag ggt ttc ctc ctt ctg gca tcc ctg agg cag atg aag 405
 Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln Met Lys
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 aag acc cgg ggc acg ctg ctg gcc ctg gag cgg aaa gac cac tct ggc 453
 Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His Ser Gly
 100 105 110
 cag gtc ttc agc gtg gtg tcc aat ggc aag gcg ggc acc ctg gac ctc 501
 Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu Asp Leu
 115 120 125 130
 agc ctg acc gtc caa gga aag cag cac gtg gtg tct gtg gaa gaa gct 549

Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu Glu Ala
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 ctc ctg gca acc ggc cag tgg aag agc atc acc ctg ttt gtg cag gaa 597
 Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val Gln Glu
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 gac agg gcc cag ctg tac atc gac tgt gaa aag atg gag aat gct gag 645
 Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn Ala Glu
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 ttg gac gtc ccc atc caa agc gtc ttc acc aga gac ctg gcc agc atc 693
 Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala Ser Ile
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 gcc aga ctc cgc atc gca aag ggg ggc gtc aat gac aat ttc cag ggg 741
 Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe Gln Gly
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 glg ctg cag aat gtg agg ttt gtc ttt gga acc aca cca gaa gac atc 789
 Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu Asp Ile
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 Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile Ser Cys
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 gat gag ctg tcc agc atg gtc ctg gaa ctc agg ggc ctg cgc acc att 981

Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg Thr Ile
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 Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu Asn Lys
 295 300 305
 gag ttg gcc aat gag ctg agg cgg cct ccc cta tgc tat cac aac gga 1077
 Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly
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 Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys Thr Glu
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 Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys Cys Pro
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 Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser Ser Val
 405 410 415

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 Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe Lys Gln
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 Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr
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 Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser
 455 460 465
 ccc cag atg aat ggg aaa ccc tgt gaa ggc gaa gcg cgg gag acc aaa 1557
 Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys
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 Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly Pro Trp
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 Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val Gln Lys
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 cgt agt cgt ctc tgc aac aac ccc gca ccc cag ttt gga ggc aag gac 1701
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 Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln Asp Cys
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 Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val Lys Cys
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 Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn
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 Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro Met Tyr
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 cgc tgc gag tgc aag cct ggc tac gct ggc aat ggc atc atc tgc ggg 2181
 Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile Cys Gly
 675 680 685 690
 gag gac aca gac ctg gat ggc tgg ccc aat gag aac ctg gtg tgc gtg 2229
 Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val Cys Val

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gcc aat gcg act tac cac tgc aaa aag gat aat tgc ccc aac ctt ccc			2277
Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn Leu Pro			
710	715	720	
aac tca ggg cag gaa gac tat gac aag gat gga att ggt gat gcc tgt			2325
Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp Ala Cys			
725	730	735	
gat gat gac gat gac aat gat aaa att cca gat gac agg gac aac tgt			2373
Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp Asn Cys			
740	745	750	
cca ttc cat tac aac cca gct cag tat gac tat gac aga gat gat gtg			2421
Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp Asp Val			
755	760	765	770
gga gac cgc tgt gac aac tgt ccc tac aac cac aac cca gat cag gca			2469
Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp Gln Ala			
775	780	785	
gac aca gac aac aat ggg gaa gga gac gcc tgt gct gca gac att gat			2517
Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp			
790	795	800	
gga gac ggt atc ctc aat gaa cgg gac aac tgc cag tac gtc tac aat			2565
Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn			
805	810	815	
gtg gac cag aga gac act gat atg gat ggg gtt gga gat cag tgt gac			2613
Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp			
820	825	830	
aat tgc ccc ttg gaa cac aat ccg gat cag ctg gac tct gac tca gac			2661
Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp			

835	840	845	850	
cgc att gga gat acc tgt gac aac aat cag gat att gat gaa gat ggc	2709			
Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly				
855	860	865		
cac cag aac aat ctg gac aac tgt ccc tat gtg ccc aat gcc aac cag	2757			
His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln				
870	875	880		
gct gac cat gac aaa gat ggc aag gga gat gcc tgt gac cac gat gat	2805			
Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp				
885	890	895		
gac aac gat ggc att cct gat gac aag gac aac tgc aga ctc gtg ccc	2853			
Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu Val Pro				
900	905	910		
aat ccc gac cag aag gac tct gac ggc gat ggt cga ggt gat gcc tgc	2901			
Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp Ala Cys				
915	920	925	930	
aaa gat gat ttt gac cat gac agt gtg cca gac atc gat gac atc tgt	2949			
Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp Ile Cys				
935	940	945		
cct gag aat gtt gac atc agt gag acc gat ttc cgc cga ttc cag atg	2997			
Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe Gln Met				
950	955	960		
att cct ctg gac ccc aaa ggg aca tcc caa aat gac cct aac tgg gtt	3045			
Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn Trp Val				
965	970	975		
gta cgc cat cag ggt aaa gaa ctc gtc cag act gtc aac tgt gat cct	3093			

Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys Asp Pro

980

985

990

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995

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His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val

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1080

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1115

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Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala			
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Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp			
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Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln			
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Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His			
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Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu			
115	120	125	
Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu			
130	135	140	
Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val			
145	150	155	160
Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn			
165	170	175	
Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala			
180	185	190	
Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe			
195	200	205	
Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu			
210	215	220	
Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu			
225	230	235	240

Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
 245 250 255
 Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
 260 265 270
 Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
 275 280 285
 Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
 290 295 300
 Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
 305 310 315 320
 Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
 325 330 335
 Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser
 340 345 350
 Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys
 355 360 365
 Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro
 370 375 380
 Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln
 385 390 395 400
 Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
 405 410 415
 Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe
 420 425 430
 Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser
 435 440 445

Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser
 450 455 460
 Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
 465 470 475 480
 Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly
 485 490 495
 Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
 500 505 510
 Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly
 515 520 525
 Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln
 530 535 540
 Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val
 545 550 555 560
 Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro
 565 570 575
 Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys
 580 585 590
 Lys Glu Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys
 595 600 605
 Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe
 610 615 620
 Thr Gly Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn
 625 630 635 640
 Lys Gln Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp
 645 650 655
 Cys Asn Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro

660	665	670	
Met Tyr Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile			
675	680	685	
Cys Gly Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val			
690	695	700	
Cys Val Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn			
705	710	715	720
Leu Pro Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp			
725	730	735	
Ala Cys Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp			
740	745	750	
Asn Cys Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp			
755	760	765	
Asp Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp			
770	775	780	
Gln Ala Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp			
785	790	795	800
Ile Asp Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val			
805	810	815	
Tyr Asn Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln			
820	825	830	
Cys Asp Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp			
835	840	845	
Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu			
850	855	860	
Asp Gly His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala			

865	870	875	880
Asn Gln Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His			
885	890	895	
Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu			
900	905	910	
Val Pro Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp			
915	920	925	
Ala Cys Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp			
930	935	940	
Ile Cys Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe			
945	950	955	960
Gln Met Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn			
965	970	975	
Trp Val Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys			
980	985	990	
Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe			
995	1000	1005	
Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly			
1010	1015	1020	
Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp			
1025	1030	1035	1040
Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln			
1045	1050	1055	
Gly Tyr Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro			
1060	1065	1070	
Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly			
1075	1080	1085	

Gln Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp

1090

1095

1100

Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe

1105

1110

1115

1120

Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly

1125

1130

1135

Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val

1140

1145

1150

Phe Ser Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg

1155

1160

1165

Asp Pro

1170

<210> 101

<211> 838

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (35).. (568)

<400> 101

gaattccgga gttttcatcc agccacgggc cagc atg tct ggg ggc aaa tac gta 55

Met Ser Gly Gly Lys Tyr Val

1

5

gac tcg gag gga cat ctc tac acc gtt ccc atc cgg gaa cag ggc aac 103

Asp Ser Glu Gly His Leu Tyr Thr Val Pro Ile Arg Glu Gln Gly Asn

10

15

20

atc tac aag ccc aac aac aag gcc atg gca gac gag ctg agc gag aag 151
 Ile Tyr Lys Pro Asn Asn Lys Ala Met Ala Asp Glu Leu Ser Glu Lys
 25 30 35
 caa gtg tac gac gcg cac acc aag gag atc gac ctg gtc aac cgc gac 199
 Gln Val Tyr Asp Ala His Thr Lys Glu Ile Asp Leu Val Asn Arg Asp
 40 45 50 55
 cct aaa cac ctc aac gat gac gtg gtc aag att gac ttt gaa gat gtg 247
 Pro Lys His Leu Asn Asp Asp Val Val Lys Ile Asp Phe Glu Asp Val
 60 65 70
 att gca gaa cca gaa ggg aca cac agt ttt cac ggc att tgg aag gcc 295
 Ile Ala Glu Pro Glu Gly Thr His Ser Phe His Gly Ile Trp Lys Ala
 75 80 85
 agc ttc acc acc ttc act gtg acg aaa tac tgg ttt tac cgc ttg ctg 343
 Ser Phe Thr Thr Phe Thr Val Thr Lys Tyr Trp Phe Tyr Arg Leu Leu
 90 95 100
 tct gcc ctc ttt ggc atc ccg atg gca ctc atc tgg ggc att tac ttc 391
 Ser Ala Leu Phe Gly Ile Pro Met Ala Leu Ile Trp Gly Ile Tyr Phe
 105 110 115
 gcc att ctc tct ttc ctg cac atc tgg gca gtt gla cca tgc att aag 439
 Ala Ile Leu Ser Phe Leu His Ile Trp Ala Val Val Pro Cys Ile Lys
 120 125 130 135
 agc ttc ctg att gag att cag tgc acc agc cgt gtc tat tcc atc tac 487
 Ser Phe Leu Ile Glu Ile Gln Cys Thr Ser Arg Val Tyr Ser Ile Tyr
 140 145 150
 gtc cac acc gtc tgt gac cca ctc ttt gaa gct gtt ggg aaa ata ttc 535
 Val His Thr Val Cys Asp Pro Leu Phe Glu Ala Val Gly Lys Ile Phe

155

160

165

agc aat gtc cgc atc aac ttg cag aaa gaa ata taaatgacat ttcaaggata 588

Ser Asn Val Arg Ile Asn Leu Gln Lys Glu Ile

170

175

gaagtatacc tgattttttt tctttttaat ttctctgggtg ccaatttcaa gtccaagtt 648

gctaatacag caacgaattt atgaattgaa ttatcttgggt tgaaaataaa aagaatcacit 708

tctcagtttt cataagtatt atgtctcttc tgagctatctt catctatctt ttggcagtcgt 768

aatttttaaa acccatitat atttctttcc ttaccttttt atttgcattgt ggaatcaacca 828

tcgctttatt

838

<210> 102

<211> 178

<212> PRT

<213> Homo sapiens

<400> 102

Met Ser Gly Gly Lys Tyr Val Asp Ser Glu Gly His Leu Tyr Thr Val

1

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Pro Ile Arg Glu Gln Gly Asn Ile Tyr Lys Pro Asn Asn Lys Ala Met

20

25

30

Ala Asp Glu Leu Ser Glu Lys Gln Val Tyr Asp Ala His Thr Lys Glu

35

40

45

Ile Asp Leu Val Asn Arg Asp Pro Lys His Leu Asn Asp Asp Val Val

50

55

60

Lys Ile Asp Phe Glu Asp Val Ile Ala Glu Pro Glu Gly Thr His Ser

65

70

75

80

Phe His Gly Ile Trp Lys Ala Ser Phe Thr Thr Phe Thr Val Thr Lys

85

90

95

Tyr Trp Phe Tyr Arg Leu Leu Ser Ala Leu Phe Gly Ile Pro Met Ala

100

105

110

Leu Ile Trp Gly Ile Tyr Phe Ala Ile Leu Ser Phe Leu His Ile Trp

115

120

125

Ala Val Val Pro Cys Ile Lys Ser Phe Leu Ile Glu Ile Gln Cys Thr

130

135

140

Ser Arg Val Tyr Ser Ile Tyr Val His Thr Val Cys Asp Pro Leu Phe

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160

Glu Ala Val Gly Lys Ile Phe Ser Asn Val Arg Ile Asn Leu Gln Lys

165

170

175

Glu Ile

<210> 103

<211> 2269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (444)

<400> 103

ccg ccc gcc acc agc tac gcc ccg tcc gac gtg ccc tcg ggg gtc gcg 48

Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala

1

5

10

15

ctg ttc ctc acc atc cct ttc gcc ttc ttc ctg ccc gag ctg ata ttt 96

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20

25

30

ggg ttc ttg gtc tgg acc atg gta gcc gcc acc cac ata gta tac ccc 144

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro
 35 40 45
 ttg ctg caa gga tgg gtg atg tat gtc tgc ctc acc tgc ttt ctc atc 192
 Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile
 50 55 60
 tcc ttg atg ttc ctg ttg tct tac ttg ttt gga ttt tac aaa aga ttt 240
 Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe
 65 70 75 80
 gaa tcc tgg aga gtt ctg gac agc ctg tac cac ggg acc act ggc atc 288
 Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile
 85 90 95
 ctg tac atg agc gct gcc gtc cta caa gta cat gcc acg att gtt tct 336
 Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser
 100 105 110
 gag aaa ctg ctg gac cca aga att tac tac att aat tgc gca gcc tgc 384
 Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser
 115 120 125
 ttc ttc gcc ttc atc gcc acg ctg ctc tac att ctc cat gcc ttc agc 432
 Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser
 130 135 140
 atc tat tac cac tga tgcacag gcgccaggcc aagggggaaa tgctcttga 484
 Ile Tyr Tyr His
 145
 aagctccaat tattgggtccc caaaagcagc ttccaacgtt tgccatctgg atgacaaacg 544
 gaagatccac taaaacgtcc acgggattaa cagaacgtcc ttgcagactg agcgatgaca 604
 ccacactttg ttggacatt taaattcact ctgctgaata ggaggaagct tttctttttc 664
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aatitagtgg tatttttagt agagatgggg ttccaccgta ttagccagga tggctctgat 1084
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aatggggagg gaaggcata gccgtcctt ccatgagct gacatctcg aaactgagca 1504
gctccggac gccgtgggtca ggaatccaag accccacctc ttaaggactg gttctcaga 1564
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attggaagaa aaggctgcc caacatctca gcgaggagt aaggacctt gtccaggaa 1684
ccgcgctg ccacctgcac tcacccccct cacattctt taagcaccg gtggccctcc 1744
gaggctggcg gaatggtggt gccacgggg ttggcaagg gtcaccagg acctcaacgg 1804
gcaaagtgt gcacactaaa atatcaaatc aagggtctg gttttaagt aaatgtttt 1864
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cgtgccctt gtcattggga atgaaataa ttattacgag aaaggacct gtccactg 1984
gtttgagcc ttacagttt gtactacat tttccctc ctgggtttg cgggacag 2044
gacagaacta caggagcat gggaaagaaa attctggtt cactactgct cactctcac 2104
ttctgatca ctctgatac ttttttttt ttttttttt gcaacctgat acctgaaaa 2164
gttctatgt gctctctt ttgtgctg gcagctgt aggatgatca ctgattacta 2224
ttactaagt agccacatgc aaataaaagt tgttggtaa aatgg 2269

<210> 104

<211> 148

<212> PRT

<213> Homo sapiens

<400> 104

Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala

1 5 10 15

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20 25 30

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro

35 40 45

Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile

50 55 60

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe

65 70 75 80

Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile

85 90 95

Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser

100 105 110

Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser

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Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser

130 135 140

Ile Tyr Tyr His

145

<210> 105

<211> 2899

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (2196)

<400> 105

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 gggccctcggc tacttggact gcggcggaat atg gcg gct ccg atg act ccc gcg 114

Met Ala Ala Pro Met Thr Pro Ala

1

5

gct cgg ccc gag gac tac gag gcg gcg ctc aat gcc gcc ctg gct gac 162
 Ala Arg Pro Glu Asp Tyr Glu Ala Ala Leu Asn Ala Ala Leu Ala Asp

10

15

20

glg ccc gaa ctg gcc aga ctc ctg gag atc gac ccg tac ttg aag ccc 210
 Val Pro Glu Leu Ala Arg Leu Leu Glu Ile Asp Pro Tyr Leu Lys Pro

25

30

35

40

tac gcc gtg gac ttc cag cgc agg tat aag cag ttt agc caa att ttg 258
 Tyr Ala Val Asp Phe Gln Arg Arg Tyr Lys Gln Phe Ser Gln Ile Leu

45

50

55

aag aac att gga gaa aat gaa ggt ggt att gat aag ttt tcc aga ggc 306
 Lys Asn Ile Gly Glu Asn Glu Gly Gly Ile Asp Lys Phe Ser Arg Gly

60

65

70

tat gaa tca ttt ggc gtc cac aga tgt gct gat ggt ggt tta tac tcc 354
 Tyr Glu Ser Phe Gly Val His Arg Cys Ala Asp Gly Gly Leu Tyr Ser

75

80

85

aaa gaa tgg gcc ccg gga gca gaa gga gtt ttt ctt act gga gat ttt 402
 Lys Glu Trp Ala Pro Gly Ala Glu Gly Val Phe Leu Thr Gly Asp Phe
 90 95 100
 aat ggt tgg aat cca ttt tcg tac cca tac aaa aaa ctg gat tat gga 450
 Asn Gly Trp Asn Pro Phe Ser Tyr Pro Tyr Lys Lys Leu Asp Tyr Gly
 105 110 115 120
 aaa tgg gag ctg tat atc cca cca aag cag aat aaa tct gta ctc gtg 498
 Lys Trp Glu Leu Tyr Ile Pro Pro Lys Gln Asn Lys Ser Val Leu Val
 125 130 135
 cct cat gga tcc aaa tta aag gta gtt att act agt aaa agc gga gag 546
 Pro His Gly Ser Lys Leu Lys Val Val Ile Thr Ser Lys Ser Gly Glu
 140 145 150
 atc ttg tat cgt att tca ccg tgg gca aag tat gtg gtt cgt gaa ggt 594
 Ile Leu Tyr Arg Ile Ser Pro Trp Ala Lys Tyr Val Val Arg Glu Gly
 155 160 165
 gat aat gtg aat tat gat tgg ata cac tgg gat cca gaa cac tca tat 642
 Asp Asn Val Asn Tyr Asp Trp Ile His Trp Asp Pro Glu His Ser Tyr
 170 175 180
 gag ttt aag cat tcc aga cca aag aag cca cgg agt cta aga att tat 690
 Glu Phe Lys His Ser Arg Pro Lys Lys Pro Arg Ser Leu Arg Ile Tyr
 185 190 195 200
 gaa tct cat gtg gga att tct tcc cat gaa gga aaa gta gct tct tat 738
 Glu Ser His Val Gly Ile Ser Ser His Glu Gly Lys Val Ala Ser Tyr
 205 210 215
 aaa cat ttt aca tgc aat gta cta cca aga atc aaa ggc ctt gga tac 786
 Lys His Phe Thr Cys Asn Val Leu Pro Arg Ile Lys Gly Leu Gly Tyr
 220 225 230

aac tgc att cag ttg atg gca atc atg gag cat gct tac tat gcc agc 834
 Asn Cys Ile Gln Leu Met Ala Ile Met Glu His Ala Tyr Tyr Ala Ser
 235 240 245
 ttt ggt tac caa atc aca agc ttc ttt gca gct tcc agc cgt tat gga 882
 Phe Gly Tyr Gln Ile Thr Ser Phe Phe Ala Ala Ser Ser Arg Tyr Gly
 250 255 260
 aca cct gaa gag cta caa gaa ctg gta gac aca gct cat tcc atg ggt 930
 Thr Pro Glu Glu Leu Gln Glu Leu Val Asp Thr Ala His Ser Met Gly
 265 270 275 280
 atc ata gtc ctc tta gat gtg gta cac agc cat gct tca aaa aat tca 978
 Ile Ile Val Leu Leu Asp Val Val His Ser His Ala Ser Lys Asn Ser
 285 290 295
 gca gat gga ttg aat atg ttt gat ggg aca gat tcc tgt tat ttt cat 1026
 Ala Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe His
 300 305 310
 tct gga cct aga ggg act cat gat ctt tgg gat agc aga ttg ttt gcc 1074
 Ser Gly Pro Arg Gly Thr His Asp Leu Trp Asp Ser Arg Leu Phe Ala
 315 320 325
 tac tcc agc tgg gaa gtt tta aga ttc ctt ctg tca aac ata aga tgg 1122
 Tyr Ser Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ile Arg Trp
 330 335 340
 tgg ttg gaa gaa tat cgc ttt gat gga ttt cgt ttt gat ggt gtt acg 1170
 Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr
 345 350 355 360
 tcc atg ctt tat cat cac cat gga gtg ggt caa ggt ttc tca ggt gat 1218
 Ser Met Leu Tyr His His His Gly Val Gly Gln Gly Phe Ser Gly Asp

365	370	375	
tac agt gaa tat ttc gga cta caa gta gat gaa gat gcc ttg act tac	1266		
Tyr Ser Glu Tyr Phe Gly Leu Gln Val Asp Glu Asp Ala Leu Thr Tyr			
380	385	390	
ctc atg ttg gca aat cat ttg gtt cac acg ctg tgt ccc gat tct ata	1314		
Leu Met Leu Ala Asn His Leu Val His Thr Leu Cys Pro Asp Ser Ile			
395	400	405	
aca ata gct gag gat gta tca gga atg cca gct ctg tgc tct cca att	1362		
Thr Ile Ala Glu Asp Val Ser Gly Met Pro Ala Leu Cys Ser Pro Ile			
410	415	420	
tcc cag gga ggg ggt ggt ttt gac tat cga cta gcc atg gca att cca	1410		
Ser Gln Gly Gly Gly Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro			
425	430	435	440
gat aag tgg att cag cta ctt aaa gag ttt aaa gat gaa gac tgg aac	1458		
Asp Lys Trp Ile Gln Leu Leu Lys Glu Phe Lys Asp Glu Asp Trp Asn			
445	450	455	
atg ggc gat ata gta tac acg ctc aca aac agg cgc tac ctt gaa aag	1506		
Met Gly Asp Ile Val Tyr Thr Leu Thr Asn Arg Arg Tyr Leu Glu Lys			
460	465	470	
tgc att gct tat gca gag agc cat gat cag gca ttg gtt ggg gat aag	1554		
Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys			
475	480	485	
tgc ctg gca ttt tgg ttg atg gat gcc gaa atg tat aca aac atg agt	1602		
Ser Leu Ala Phe Trp Leu Met Asp Ala Glu Met Tyr Thr Asn Met Ser			
490	495	500	
gtc ctg act cct ttt act cca gtt att gat cgt gga ata cag ctt cat	1650		
Val Leu Thr Pro Phe Thr Pro Val Ile Asp Arg Gly Ile Gln Leu His			

505	510	515	520	
aaa atg att cga ctc att acg cat ggg ctt ggt gga gaa ggc tat ctc				1698
Lys Met Ile Arg Leu Ile Thr His Gly Leu Gly Gly Glu Gly Tyr Leu				
525	530	535		
aat ttc atg ggt aat gaa ttt ggg cat cct gaa tgg tta gac ttc cca				1746
Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Leu Asp Phe Pro				
540	545	550		
aga aaa gga aat aat gag agt tac cat tat gcc agg cgg cag ttt cat				1794
Arg Lys Gly Asn Asn Glu Ser Tyr His Tyr Ala Arg Arg Gln Phe His				
555	560	565		
tta act gac gac gac ctt ctt cgc tac aag ttc cta aat aat ttt gac				1842
Leu Thr Asp Asp Asp Leu Leu Arg Tyr Lys Phe Leu Asn Asn Phe Asp				
570	575	580		
agg gat atg aat aga ttg gaa gaa aga tat ggt tgg ctt gca gct cca				1890
Arg Asp Met Asn Arg Leu Glu Glu Arg Tyr Gly Trp Leu Ala Ala Pro				
585	590	595	600	
cag gcc tac gtg agt gaa aaa cat gaa ggc aat aag atc att gct ttt				1938
Gln Ala Tyr Val Ser Glu Lys His Glu Gly Asn Lys Ile Ile Ala Phe				
605	610	615		
gaa aga gca ggt ctt ctt ttc att ttc aac ttc cat cca agc aag agc				1986
Glu Arg Ala Gly Leu Leu Phe Ile Phe Asn Phe His Pro Ser Lys Ser				
620	625	630		
tac act gac tac cga gtt gga aca gca ttg cca ggg aaa ttc aaa att				2034
Tyr Thr Asp Tyr Arg Val Gly Thr Ala Leu Pro Gly Lys Phe Lys Ile				
635	640	645		
gtg cta gat tca gat gca gcg gaa tat gga ggg cat cag aga ctg gac				2082

Val Leu Asp Ser Asp Ala Ala Glu Tyr Gly Gly His Gln Arg Leu Asp

650

655

660

cac agc act gac ttt ttt tct gag gct ttt gaa cat aat ggg cgt ccc 2130

His Ser Thr Asp Phe Phe Ser Glu Ala Phe Glu His Asn Gly Arg Pro

665

670

675

680

tat tct ctt ttg gtg tac att cca agc aga gtg gcc ctc atc ctt cag 2178

Tyr Ser Leu Leu Val Tyr Ile Pro Ser Arg Val Ala Leu Ile Leu Gln

685

690

695

aat gtg gat ctg ccg aat tgaagaggcc tgatttcagc tccaccagat 2226

Asn Val Asp Leu Pro Asn

700

gcagatttgt gttttgtttt ctgtttatca ctgtcacaca gcttataaca tgtatgcttt 2286

tcagaatata gttgtctagc caagccatca agtgtctgaa attcaatatt ggtttatgca 2346

aatacagcaa acttttatTT aagtagatag gagaatatgt ttaaaatatt aggaatccta 2406

gaccatatTT tcaagtcate tttagcagcta ggattctcaa atggaagtgt tatatataat 2466

atgttaaaaa cattttgctt tcttggttaa ttatttgatc ctttlaaatc caaatttgaa 2526

tcatttgtea tgtatgatta tttctgttaa atgtacacag tatttaagat ggatatitgg 2586

tggctctatt tgtctgata tcttttggc taaattatga ggtaccaaga ttgtttcttt 2646

gtttcttttt ttcaaattgt gtttagaaat actglaataa atalgcagta gtgatataaa 2706

gaattataic caaggtaata taaaagccat tacglaigaa cicalccgtg tctcatitig 2766

tgttttatTT tgtgatctct tgtccactaa gtaetltgtt aaatgccagt atctcagctt 2826

ttctgaagcc ctgaaatggt aattgtagca tttcagaaaa tgtctttcat ttcaatcaat 2886

aaaaagcttt tgt 2899

<210> 106

<211> 702

<212> PRT

<213> Homo sapiens

<400> 106

Met Ala Ala Pro Met Thr Pro Ala Ala Arg Pro Glu Asp Tyr Glu Ala

1 5 10 15

Ala Leu Asn Ala Ala Leu Ala Asp Val Pro Glu Leu Ala Arg Leu Leu

20 25 30

Glu Ile Asp Pro Tyr Leu Lys Pro Tyr Ala Val Asp Phe Gln Arg Arg

35 40 45

Tyr Lys Gln Phe Ser Gln Ile Leu Lys Asn Ile Gly Glu Asn Glu Gly

50 55 60

Gly Ile Asp Lys Phe Ser Arg Gly Tyr Glu Ser Phe Gly Val His Arg

65 70 75 80

Cys Ala Asp Gly Gly Leu Tyr Ser Lys Glu Trp Ala Pro Gly Ala Glu

85 90 95

Gly Val Phe Leu Thr Gly Asp Phe Asn Gly Trp Asn Pro Phe Ser Tyr

100 105 110

Pro Tyr Lys Lys Leu Asp Tyr Gly Lys Trp Glu Leu Tyr Ile Pro Pro

115 120 125

Lys Gln Asn Lys Ser Val Leu Val Pro His Gly Ser Lys Leu Lys Val

130 135 140

Val Ile Thr Ser Lys Ser Gly Glu Ile Leu Tyr Arg Ile Ser Pro Trp

145 150 155 160

Ala Lys Tyr Val Val Arg Glu Gly Asp Asn Val Asn Tyr Asp Trp Ile

165 170 175

His Trp Asp Pro Glu His Ser Tyr Glu Phe Lys His Ser Arg Pro Lys

180 185 190

Lys Pro Arg Ser Leu Arg Ile Tyr Glu Ser His Val Gly Ile Ser Ser

195	200	205	
His Glu Gly Lys Val Ala Ser Tyr Lys His Phe Thr Cys Asn Val Leu			
210	215	220	
Pro Arg Ile Lys Gly Leu Gly Tyr Asn Cys Ile Gln Leu Met Ala Ile			
225	230	235	240
Met Glu His Ala Tyr Tyr Ala Ser Phe Gly Tyr Gln Ile Thr Ser Phe			
	245	250	255
Phe Ala Ala Ser Ser Arg Tyr Gly Thr Pro Glu Glu Leu Gln Glu Leu			
260	265	270	
Val Asp Thr Ala His Ser Met Gly Ile Ile Val Leu Leu Asp Val Val			
275	280	285	
His Ser His Ala Ser Lys Asn Ser Ala Asp Gly Leu Asn Met Phe Asp			
290	295	300	
Gly Thr Asp Ser Cys Tyr Phe His Ser Gly Pro Arg Gly Thr His Asp			
305	310	315	320
Leu Trp Asp Ser Arg Leu Phe Ala Tyr Ser Ser Trp Glu Val Leu Arg			
	325	330	335
Phe Leu Leu Ser Asn Ile Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp			
340	345	350	
Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His His His Gly			
355	360	365	
Val Gly Gln Gly Phe Ser Gly Asp Tyr Ser Glu Tyr Phe Gly Leu Gln			
370	375	380	
Val Asp Glu Asp Ala Leu Thr Tyr Leu Met Leu Ala Asn His Leu Val			
385	390	395	400
His Thr Leu Cys Pro Asp Ser Ile Thr Ile Ala Glu Asp Val Ser Gly			

405	410	415	
Met Pro Ala Leu Cys Ser Pro Ile Ser Gln Gly Gly Gly Gly Phe Asp			
420	425	430	
Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile Gln Leu Leu Lys			
435	440	445	
Glu Phe Lys Asp Glu Asp Trp Asn Met Gly Asp Ile Val Tyr Thr Leu			
450	455	460	
Thr Asn Arg Arg Tyr Leu Glu Lys Cys Ile Ala Tyr Ala Glu Ser His			
465	470	475	480
Asp Gln Ala Leu Val Gly Asp Lys Ser Leu Ala Phe Trp Leu Met Asp			
485	490	495	
Ala Glu Met Tyr Thr Asn Met Ser Val Leu Thr Pro Phe Thr Pro Val			
500	505	510	
Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile Arg Leu Ile Thr His			
515	520	525	
Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly			
530	535	540	
His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly Asn Asn Glu Ser Tyr			
545	550	555	560
His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp Asp Asp Leu Leu Arg			
565	570	575	
Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met Asn Arg Leu Glu Glu			
580	585	590	
Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr Val Ser Glu Lys His			
595	600	605	
Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala Gly Leu Leu Phe Ile			
610	615	620	

Phe Asn Phe His Pro Ser Lys Ser Tyr Thr Asp Tyr Arg Val Gly Thr

625 630 635 640

Ala Leu Pro Gly Lys Phe Lys Ile Val Leu Asp Ser Asp Ala Ala Glu

645 650 655

Tyr Gly Gly His Gln Arg Leu Asp His Ser Thr Asp Phe Phe Ser Glu

660 665 670

Ala Phe Glu His Asn Gly Arg Pro Tyr Ser Leu Leu Val Tyr Ile Pro

675 680 685

Ser Arg Val Ala Leu Ile Leu Gln Asn Val Asp Leu Pro Asn

690 695 700

<210> 107

<211> 790

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78).. (626)

<400> 107

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tctccttagt cgccgcc atg acg acc gcg tcc acc tcg cag gtg cgc cag 110

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln

1 5 10

aac tac cac cag gac tca gag gcc gcc atc aac cgc cag atc aac ctg 158

Asn Tyr His Gln Asp Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu

15 20 25

gag ctc tac gcc tcc tac gtt tac ctg tcc atg tct tac tac ttt gac 206

Glu Leu Tyr Ala Ser Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp
 30 35 40
 cgc gat gat gtg gct ttg aag aac ttt gcc aaa tac ttt ctt cac caa 254
 Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln
 45 50 55
 tct cat gag gag agg gaa cat gct gag aaa ctg atg aag ctg cag aac 302
 Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn
 60 65 70 75
 caa cga ggt ggc cga atc ttc ctt cag gat atc aag aaa cca gac tgt 350
 Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys
 80 85 90
 gat gac tgg gag agc ggg ctg aat gca atg gag tgt gca tta cat ttg 398
 Asp Asp Trp Glu Ser Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu
 95 100 105
 gaa aaa aat gtg aat cag tca cta ctg gaa ctg cac aaa ctg gcc act 446
 Glu Lys Asn Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr
 110 115 120
 gac aaa aat gac ccc cat ttg tgt gac ttc att gag aca cat tac ctg 494
 Asp Lys Asn Asp Pro His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu
 125 130 135
 aat gag cag gtg aaa gcc atc aaa gaa ttg ggt gac cac gtg acc aac 542
 Asn Glu Gln Val Lys Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn
 140 145 150 155
 ttg cgc aag atg gga gcg ccc gaa tct ggc ttg gcg gaa tat ctc ttt 590
 Leu Arg Lys Met Gly Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe
 160 165 170

gac aag cac acc ctg gga gac agt gat aat gaa agc taagcctcgg 636

Asp Lys His Thr Leu Gly Asp Ser Asp Asn Glu Ser

175

180

gctaatttcc ccatagccgt ggggtgactt ccttggtcac caaggcagtg catgcatgtt 696

ggggtttccct ttaccttttc tataagtgt accaaaacat ccacttaagt tctttgattt 756

gtaccattcc ttcaaataaa gaaatttggt accc 790

<210> 108

<211> 183

<212> PRT

<213> Homo sapiens

<400> 108

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln Asn Tyr His Gln Asp

1

5

10

15

Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser

20

25

30

Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp Arg Asp Asp Val Ala

35

40

45

Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln Ser His Glu Glu Arg

50

55

60

Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn Gln Arg Gly Gly Arg

65

70

75

80

Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys Asp Asp Trp Glu Ser

85

90

95

Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu Glu Lys Asn Val Asn

100

105

110

Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn Asp Pro

115 120 125
 His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys
 130 135 140
 Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly
 145 150 155 160
 Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe Asp Lys His Thr Leu
 165 170 175
 Gly Asp Ser Asp Asn Glu Ser
 180

<210> 109

<211> 3460

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (256).. (1857)

<400> 109

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 gggctgggct gtgcgcctgc gcagtgtggg tcgctccga ttccctgccc cggccggccc 180
 cgctcggt cgcacccctc gcccgcctct cagccgcgc tctgccccgc agcagccagc 240
 cccgtgtccg gcagt atg ttc agc tgg gtc agc aag gat gcc cgc cgc aag 291

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys

1

5

10

aag gag ccg gag ctc ttc cag acg gtg gcc gag ggg ctg cgg cag ctg 339
 Lys Glu Pro Glu Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu

15	20	25	
tac gcg cag aag ctg cta ccc ctg gag gag cac tac cgc ttc cac gag	387		
Tyr Ala Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu			
30	35	40	
ttc cac tcg ccc gcr ctg gag gac gct gac ttc gac aac aag cct atg	435		
Phe His Ser Pro Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met			
45	50	55	60
gtg ctc ctc gtg rgg cag tac agc acg ggc aag acc acc ttc atc cga	483		
Val Leu Leu Val Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg			
65	70	75	
cac ctg atc gag cag gac ttc ccg ggg atg cgc atc ggg ccc gag ccc	531		
His Leu Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro			
80	85	90	
acc acc gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc gtg	579		
Thr Thr Asp Ser Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val			
95	100	105	
gtg ccg ggc aac gcg ctc gtg gtg gac ccg cgg cgc ccc ttc cgc aag	627		
Val Pro Gly Asn Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys			
110	115	120	
ctc aac gcg ttt ggc aac gct ttc ctc aac agg ttc atg tgt gcc cag	675		
Leu Asn Ala Phe Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln			
125	130	135	140
ctg ccc aac ccc gtc ctg gac agc atc agc atc atc gac acc ccc ggg	723		
Leu Pro Asn Pro Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly			
145	150	155	
atc ctg tct gga gag aag cag cgg atc agc aga ggc tal gac ttt gca	771		
Ile Leu Ser Gly Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala			

160	165	170	
gcc gtc ctg gag tgg ttc gcg gag cgt gtg gac cgc atc atc ctg ctc	819		
Ala Val Leu Glu Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu			
175	180	185	
ttc gac gcc cac aag ctg gac atc tcc gat gag ttc tcg gaa gtg atc	867		
Phe Asp Ala His Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile			
190	195	200	
aag gct ctg aag aac cat gag gac aag atc cgc gtg gtg ctg aac aag	915		
Lys Ala Leu Lys Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys			
205	210	215	220
gca gac cag atc gag acg cag cag ctg atg cgg gtg tac ggg gcc ctc	963		
Ala Asp Gln Ile Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu			
225	230	235	
atg tgg tcc ctg ggc aag atc atc aac acc ccc gag gtg gtc agg gtc	1011		
Met Trp Ser Leu Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val			
240	245	250	
tac atc ggc tcc ttc tgg tcc cac ccg ctc ctc atc ccc gac aac cgc	1059		
Tyr Ile Gly Ser Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg			
255	260	265	
aag ctc ttt gag gcc gag gag cag gac ctc ttc aag gac atc cag tca	1107		
Lys Leu Phe Glu Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser			
270	275	280	
ctg ccc cga aac gcc gcc ctc agg aag ctc aat gac ctg atc aag cgg	1155		
Leu Pro Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg			
285	290	295	300
gca cgg ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa	1203		

Ala Arg Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys
 305 310 315
 gag atg ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg 1251
 Glu Met Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val
 320 325 330
 aac aac ctg gga gag atc tac cag aag att gag cgc gag cac cag atc 1299
 Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile
 335 340 345
 tcc cct ggg gac ttc ccg agc ctc cgc aag atg cag gaa ctc ctg cag 1347
 Ser Pro Gly Asp Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln
 350 355 360
 acc cag gac ttc agc aag ttc cag gcg ctg aag ccc aag ctg ctg gac 1395
 Thr Gln Asp Phe Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp
 365 370 375 380
 acg gtg gat gac atg ctg gcc aac gac atc gcg cgg ctg atg gtg atg 1443
 Thr Val Asp Asp Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met
 385 390 395
 gtg cgg cag gag gag tcc ctg atg cct tcc cag gtg gtc aag ggc ggc 1491
 Val Arg Gln Glu Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly
 400 405 410
 gcc ttt gac ggc acc atg aac ggg ccg ttc ggg cac ggc tac ggc gag 1539
 Ala Phe Asp Gly Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu
 415 420 425
 ggg gcc ggc gag ggc atc cac gac gtg gag tgg gtg gtg ggc aag gac 1587
 Gly Ala Gly Glu Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp
 430 435 440
 aag ccc acc tac gac gag atc ttc tac acg ctg tcc cct gtc aac ggc 1635

Lys Pro Thr Tyr Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly
 445 450 455 460
 aag atc acg ggc gcc aac gcc aag aag gag atg gtg aag tcc aag ctc 1683
 Lys Ile Thr Gly Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu
 465 470 475
 ccc aac acc gtg cta ggg aag atc tgg aag ctg gcc gac gtg gac aag 1731
 Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys
 480 485 490
 gac ggg ctg ctg gac gac gag gag ttc gcg ctg gcc aac cac ctc atc 1779
 Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile
 495 500 505
 aag gtc aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac 1827
 Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His
 510 515 520
 ctg gtg ccg ccc tcc aag cgc aga cat gag tga tggcgc cggccccgca 1877
 Leu Val Pro Pro Ser Lys Arg Arg His Glu
 525 530
 cc tgc cca ttt gca cgc ccc ggc cc ggg gag gca gag ac ggg gg gag gg ga agc ctc acc att t 1937
 ctc aag gtc ataa ag actg agc gat gtt tcc tgc ctc tcg aaa agga aa acc acc at 1997
 ctt tct ttt a agc tgc ttc tgg cc tgc ggg gg gag gca ggg gtg ag ag gat gga att g 2057
 tgc tca ca ag aac tgc tgc at ttt aat at ata ac gtt ag agc tgc gtt ctt tgc c 2117
 gcc tccc ctg tgc cag cc ctg tgc ac gcc tgc cccc gg cc tt gtc tgc tgc 2177
 tgg ag ctg ga cag tgc ag tgc ac tgc gac cc tgg gg gag cc ag tgc cc ct ttc ggc ag ct 2237
 gct ag gct ga ggc tgc at gg ac ag ga ac ac cag gc acc ct cc gtc tgc tt ctg ag ctg ag 2297
 gtt gct tca cgg acc gtc ctt ctt cct cacc tgc tgc tgc tcccc gtc tgc tgc 2357
 gc ga ag tgg tct tgc tccc tccc gg gcc ag gc tccc gtc cgg gcc ctg 2417

cctttctctc cgcgccccac cggctccgac gcgcaacccc gctcagcagt cacagaagca 2477
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 ccgtacttcc atacagtatt aggtgaggat ggatcggggc gctgtccttg ccgggaagtc 3377
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 tgcattaaaa agtctgaact gtc 3460

<210> 110

<211> 534

<212> PRT

<213> Homo sapiens

<400> 110

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys Lys Glu Pro Glu

1

5

10

15

Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu Tyr Ala Gln Lys

20	25	30	
Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu Phe His Ser Pro			
35	40	45	
Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu Leu Val			
50	55	60	
Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu Ile Glu			
65	70	75	80
Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr Asp Ser			
85	90	95	
Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro Gly Asn			
100	105	110	
Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn Ala Phe			
115	120	125	
Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Pro			
130	135	140	
Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly			
145	150	155	160
Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala Ala Val Leu Glu			
165	170	175	
Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu Phe Asp Ala His			
180	185	190	
Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile Lys Ala Leu Lys			
195	200	205	
Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Gln Ile			
210	215	220	
Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ser Leu			
225	230	235	240

Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser			
245	250	255	
Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu			
260	265	270	
Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn			
275	280	285	
Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala			
290	295	300	
Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn			
305	310	315	320
Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly			
325	330	335	
Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp			
340	345	350	
Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe			
355	360	365	
Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp			
370	375	380	
Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu			
385	390	395	400
Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly			
405	410	415	
Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu			
420	425	430	
Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr			
435	440	445	

Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly

450

455

460

Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val

465

470

475

480

Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys Asp Gly Leu Leu

485

490

495

Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile Lys Val Lys Leu

500

505

510

Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val Pro Pro

515

520

525

Ser Lys Arg Arg His Glu

530

<210> 111

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89).. (724)

<400> 111

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gtgtgattaa cctccatttc agctaatac atg gga gag att aaa gtc tct cct 112

Met Gly Glu Ile Lys Val Ser Pro

1

5

gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg 160

Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val

10	15	20	
gat gat gat gac agt aag ata tgg tgc ctc tat gac gcg ggc ccc cga			208
Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg			
25	30	35	40
agt atc agg tgt cct ctc ata ttc ctg ccc cct gtc agt gga act gca			256
Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala			
45	50	55	
gat gtc ttt ttc cgg cag att ttg gct ctg act gga tgg ggt tac cgg			304
Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg			
60	65	70	
gtt atc gct ttg cag tat cca gtt tat tgg gac cat ctc gag ttc tgt			352
Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys			
75	80	85	
gat gga ttc aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat			400
Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His			
90	95	100	
ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa			448
Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu			
105	110	115	120
tac act cac aaa tct cct aga gtc cat tcc cta atc ctc tgc aat tcc			496
Tyr Thr His Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser			
125	130	135	
ttc agt gac acc tct atc ttc aac caa act tgg act gca aac agc ttt			544
Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe			
140	145	150	
tgg ctg atg cct gca ttt atg ctc aaa aaa ala gtt ctt gga aat ttt			592
Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe			

155	160	165	
tca tct ggc ccg gtg gac cct atg atg gct gat gcc att gat ttc atg			640
Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met			
170	175	180	
gta gac agg cta gaa agt ttg ggt cag agt gaa ctg gct tca aga ctt			688
Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu			
185	190	195	200
acc ttg aaa ttg tca aaa ttc tta tgt gga acc tca taaaattcgg			734
Thr Leu Lys Leu Ser Lys Phe Leu Cys Gly Thr Ser			
205	210		
ggacatacct gtaactattt tggatgtgtt tgatcagagt gcgctttcaa ctgaagctaa			794
agaagaaatg tacaagctgt atccctaattg ccccgagag gctcatctga aaacaggagg			854
caatttccca taccgtgtca gaagtcaga ggtcaatctt tatgtacaga tacatttgc			914
kgcaattccw kggrggaccm aatacgcggc ctttgacca tcaatggta gtcggagga			974
gcttgaggig cagaaaggca gccttggcat cagccaggag gagcagtagt gtgtctctcg			1034
ctgtcaatga tgagtigacc cggltgttgc ttgtatagtc agtgggcac agcacccgtt			1094
cagccggcct ttccctcag gttcgtcagg ctcaccggtt ctcactgtgt ctgggaagta			1154
ggactgaagg tcaatctcat gacaggcggc atctccacta agcctgtgta actgttccct			1214
ctttggtttt cttagctttt gaattigaag aagtaattt gaagacccc atttlaagaa			1274
ccgtgcaaat ttgtctacca aaagcttca ccactgtgtt cttaagtga tgtaatttc			1334
tgaggtttgg gactttgtgg tggttttttt cttctttct ttccattct tctttcttc			1394
tttttatgtt gtttgcgtga aatgctgcac atccagattg catatcagga catggttat			1454
tttatgcttt ctggatata accatgatca gaggccatg gccactacc cactgtttgc			1514
tctctgcaa atcaactgtt tttaatttac acttaaacaa attgttttga gtgttagcta			1574
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<211> 212

<212> PRT

<213> Homo sapiens

<400> 112

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr

1 5 10 15

Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Asp Ser Lys Ile Trp

20 25 30

Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe

35 40 45

Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu

50 55 60

Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val

65 70 75 80

Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp

85 90 95

His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly

100 105 110

Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val

115 120 125

His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn

130 135 140

Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu

145 150 155 160

Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met

165 170 175

Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly

180

185

190

Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Lys Leu Ser Lys Phe Leu

195

200

205

Cys Gly Thr Ser

210

<210> 113

<211> 2391

<212> DNA

<213> Homo sapiens

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<222> (1705)

<223> g or t

<400> 113

gac ccg ttc cat gca gtt gta tac ata gtg ttc atg ctg ggc tcc tgt 48

Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

1

5

10

15

kcw tty kkc tcc aaa acg tgg att gag gtc tca ggt tcc tct scc aaa 96

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

gat gyt kca aag cag ctg aag gag cag cag atg gtg atg aga ggc cac 144

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35

40

45

cga gag acc tcc atg gtc cat gaa ctc aac cgg tac atc ccc aca gcc 192

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50

55

60

gcg gcc ttt ggt ggg ctg tgc atc ggg gcc ctc tcg gtc ctg gct gac 240

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp
 65 70 75 80
 ttc cta ggc gcc att ggg tct gga acc ggg atc ctg ctc gca gtc aca 288
 Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr
 85 90 95
 atc atc tac cag tac ttt gag atc ttc gtt aag gag yaa agc gag gtt 336
 Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val
 100 105 110
 ggc agc atg ggg gcc ctg ctc ttc tgagcccgct tcccgacag gttgaggaag 390
 Gly Ser Met Gly Ala Leu Leu Phe
 115 120
 ctgctccaga agcgctcgg aagggagct ctacatgg cgcgtgctgc tgcggcatat 450
 ggacttttaa taatgtgttt tgaatttcgt attctttcat tccactgtgt aaagtgciaa 510
 acattttcca atttaaaatt ttgcttttta tccctggcact ggcaaaaaga actgtgaaag 570
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caccaccgac ttccittctg cgtcaccagt gtcgtcagca gagagaggac agcacaggct 1410
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 acactcacgc cctgtgggtg atggcacagg tgggtgggtg ggggctgacc ccagcttcca 2310
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 taaagccagt tttttacaag g 2391

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<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (17)

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<222> (31)

<223> unknown

<220>

<221> unsure

<222> (109)

<223> unknown

<400> 114

Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

1

5

10

15

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35

40

45

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50

55

60

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp

65	70	75	80
Phe	Leu	Gly	Ala
Ile	Gly	Ser	Gly
Thr	Gly	Ile	Leu
Leu	Ala	Val	Thr
85	90	95	
Ile	Ile	Tyr	Gln
Tyr	Phe	Glu	Ile
Phe	Val	Lys	Glu
Xaa	Ser	Glu	Val
100	105	110	
Gly	Ser	Met	Gly
Ala	Leu	Leu	Phe
115	120		

<210> 115

<211> 599

<212> DNA

<213> Homo sapiens

<400> 115

gggtatggaa ttggctgagg atcaaacgta tgtaggtaga aggataccag gatgttgcta 60
 aaggtgaggg acagttiggg ttggggactt accggggtaga tgtagaact ggaacccccca 120
 agtgaggctg gagggagtta aggtcagtat ggaagatagg gtggggacag ggtgctttgg 180
 aatgaaagag tgacctaga gggctccttg ggcctcagga atgctcctgc tgctgtgaag 240
 atgagaaggt gctcttactc agttaatgat gaggactat attacccaaa gcccctacct 300
 gctgctgggt cccttgtagc acaggagact tgggctaagg gcccctccca gggaaggac 360
 accatcagge cctggtgta ggcagtagca tagaggatcc attctacct gcattccca 420
 gaggactagc aggaggcagc ctgagaaaac cggcagttcc caaagccagc gcctggcigt 480
 tctctcattg tcactgccct ccccccaacc tctctctaa cccactagag attgccigtg 540
 tctgccctct tgcctcttgt agaatgcagc tctggccctc aataaatgct tctgcatt 599

<210> 116

<211> 364

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (134)

<223> a, c, g or t

<220>

<221> unsure

<222> (135)

<223> a, c, g or t

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<221> unsure

<222> (179)

<223> g or a

<400> 116

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acagtgcctc caggggtgca ttggtgggaa tgagaatagt gatgaagtag aaatgtctgc 120

cacagtcca ggannggga gglagcagtg tgtgtgttat gtgccactga cctgaaara 180

tgtgccatag cccaagccaa ttgaaatga tcagggggcc aggcatggcg gctcatgcct 240

glaatcccag caccttggga agctgaggtg ggaggattgc ttgaaaccag gagttcaaga 300

ccagcctgtg caacatagca aaaccccatc tclacaaaga ttaaaaataa aaaattagct 360

gggc

364

<210> 117

<211> 852

<212> DNA

<213> Homo sapiens

<220>

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<222> (26).. (217)

<220>

<221> unsure

<222> (37)

<223> a. c. g or t

<400> 117

gttcagtttc aagtttacia gaggc atg gat gga gln gtg acg ttc ttg aca 52

Met Asp Gly Xaa Val Thr Phe Leu Thr

1

5

agc tgg gct aac ctt tcc cga act tgt ttc ccg gag gca agg tgc tgc 100

Ser Trp Ala Asn Leu Ser Arg Thr Cys Phe Pro Glu Ala Arg Cys Ser

10

15

20

25

gtg acc cag cgc atc tta acc ttg ggt ctc cta ggc tgc agg cta ggg 148

Val Thr Gln Arg Ile Leu Thr Leu Gly Leu Leu Gly Ser Arg Leu Gly

30

35

40

cat tac gtt tgc tgg aac caa agc agc caa ttg cat agc aag tat ttt 196

His Tyr Val Ser Trp Asn Gln Ser Ser Gln Leu His Ser Lys Tyr Phe

45

50

55

cct gca ttc caa tta aat gct taagaaaaag cagcatccta taaaattgtg 247

Pro Ala Phe Gln Leu Asn Ala

60

atcataaaca tccatttccc tcagcttttg tgagtgcctt gacttacagc caacatcact 307
 gttaaactca gtctgtttaa aaacaaactt ttctgggtgt tgataacaga gatttgctcc 367
 ctgagccatc agggctcctgg gagctggaag tgaaagggtt attaacattc taccittatg 427
 cagctgttgg ctgaccagaa taaactccct gctgagttca agcttligaat ggaatggatg 487
 caaatgatgt tgtttccatt agagcaggtg ctacacagcat tctgattggc ctgagcagac 547
 cgaggctatg gctgttggga caagcttagc atcctggaca tcttgtcaaa gaaccicact 607
 caccctctcg gcctctacag ccctcagagg agagaaaacc aattctccaa caaacaggtc 667
 tcaccaacat ggtgglgctg gcaggcttag gtttagaaaa tctgactgt taaaggcgtt 727
 tgaatacatc acattcctat gcaaatgttt ttaatctcca gttaaataa gtttattttt 787
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 gaagc 852

<210> 118

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (4)

<223> unknown

<400> 118

Met Asp Gly Xaa Val Thr Phe Leu Thr Ser Trp Ala Asn Leu Ser Arg

1

5

10

15

Thr Cys Phe Pro Glu Ala Arg Cys Ser Val Thr Gln Arg Ile Leu Thr

20

25

30

Leu Gly Leu Leu Gly Ser Arg Leu Gly His Tyr Val Ser Trp Asn Gln

35

40

45

Ser Ser Gln Leu His Ser Lys Tyr Phe Pro Ala Phe Gln Leu Asn Ala

50

55

60

<210> 119

<211> 1156

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (524)... (1105)

<220>

<221> unsure

<222> (10)

<223> a or t

<400> 119

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 gctagagaca gggagagcag aglaaaaccc tcaggcigtct gaaattticta ggctgttagg 180
 aagcccctcg aattctgtga aatgagggt ttcttaactc acactgagag cggaaagggg 240
 cagacccttt tcataactcc ctcaagtggtg tgttaccttt ctttaccagc atggttaagca 300
 acaggacata tcccagcctc ggacatgict gtagatcca aggtacccaa agtcagacag 360
 aglaaactca agcctggcac tggctttctg ccgcttcatg tgctttggaa aaagcaggag 420
 aagcaatagc agcaggagtc cccagcagct ggagccgcaa gaatgaactg caaagaggga 480
 actgacagca gctgcggctg cagggggcaa cgacgagaag aag atg ttg aag tgt 535

Met Leu Lys Cys

1

gtg gtg gtg ggg gac ggt gcc gtg ggg aaa acc tgc ctg ctg atg agc 583
 Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Met Ser
 5 10 15 20
 tac gcc aac gac gcc ttc cca gag gaa tac gtg ccc act gtg ttt gac 631
 Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro Thr Val Phe Asp
 25 30 35
 cac tat gca gtt act gtg act gtg gga ggc aag caa cac ttg ctc gga 679
 His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln His Leu Leu Gly
 40 45 50
 ctg tat gac acc gcg gga cag gag gac tac aac cag ctg agg cca ctc 727
 Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln Leu Arg Pro Leu
 55 60 65
 tcc tac ccc aac acg gat gtg ttt ttg atc tgc ttc tct gtc gta aac 775
 Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn
 70 75 80
 cct gcc tct tac cac aat gtc cag gag gaa tgg gtc ccc gag ctc aag 823
 Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val Pro Glu Leu Lys
 85 90 95 100
 gac tgc atg cct cac gtg cct tat gtc ctc ata ggg acc cag att gat 871
 Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly Thr Gln Ile Asp
 105 110 115
 ctc cgt gat gac cca aaa acc ttg gcc cgt ttg ctg tat atg aaa gag 919
 Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu Tyr Met Lys Glu
 120 125 130
 aaa cct ctc act tac gag cat ggt gtg aag ctc gca aaa gcg atc gga 967
 Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala Lys Ala Ile Gly

135	140	145	
gca cag tgc tac ttg gaa tgt tca gct ctg act cag aaa ggt ctc aaa			1015
Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys			
150	155	160	
gcg gtt ttt gat gaa gca atc ctc acc att ttc cac ccc aag aaa aag			1063
Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His Pro Lys Lys Lys			
165	170	175	180
aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca att atc			1105
Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser Ile Ile			
185	190		
tgaggttgtc tgggaccigc ctccacccca tccagggatg agaatggcag c			1156

<210> 120

<211> 194

<212> PRT

<213> Homo sapiens

<400> 120

Met Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys

1	5	10	15
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Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro

20	25	30
----	----	----

Thr Val Phe Asp His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln

35	40	45
----	----	----

His Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln

50	55	60
----	----	----

Leu Arg Pro Leu Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe

65	70	75	80
----	----	----	----

Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val

85

90

95

Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly

100

105

110

Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu

115

120

125

Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala

130

135

140

Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln

145

150

155

160

Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His

165

170

175

Pro Lys Lys Lys Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser

180

185

190

Ile Ile

<210> 121

<211> 1732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (259)

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<221> unsure

<222> (28)

<223> a, c, g or t

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<222> (388)

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<222> (631)

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<222> (637)

<223> g or a

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<222> (638)

<223> g or a

<220>

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<222> (639)

<223> g or a

<400> 121

g gac att gag tcc aag gag cag gtg cgn acc ctc acg ggc cac gtg ggc 49

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

acc gtg tat gcc ctg gcg gtc atc tcg acg cca gac cag acc aaa gtc 97

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20	25	30	
ttc agt gca tcc tac gac cgg tcc ctc agg gtc tgg agt atg gac aac	145		
Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn			
35	40	45	
atg atc tgc acg cag acc ctg ctg cgt cac cag ggc agt gtc acc gcg	193		
Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala			
50	55	60	
ctg gct gtg tcc cgg ggc cga ctc ttc tca ggg gct gtg gat agc act	241		
Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr			
65	70	75	80
gtg aag gtt tgg act tgc taacaggatc caggccaggc tgtggtttcc	289		
Val Lys Val Trp Thr Cys			
85			
ccigaaccag cccigggacct ttctgagcca ggctggccac atgggggtggt ctcggggttt	349		
ctgctgccc cgtgggcata ggtggacagg ctctggcarg ccggcagtc cctccccgc	409		
ccatgctcgg cgagcctccc tctacteggc actgtccttg ctgcccagcc cctctctggg	469		
tgccaggtae gacgcttgcc ccggcccacc ctccatcccc accctccatc cccaccctag	529		
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<210> 122

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (9)

<223> unknown

<400> 122

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20

25

30

Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn

35

40

45

Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala

50

55

60

Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr

65

70

75

80

Val Lys Val Trp Thr Cys

85

<210> 123

<211> 603

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<213> Homo sapiens

<220>

<221> CDS

<222> (168).. (350)

<220>

<221> unsure

<222> (343)

<223> g or a

<220>

<221> unsure

<222> (422)

<223> t or c

<220>

<221> unsure

<222> (457)

<223> g or c

<400> 123

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 gccaaacttg gtgaagact aggtcttccc tggcaagtgc cggaaga atg gac tta 176

Met Asp Leu

1

ctg act ttt atc aac tct tct cac tgc caa ggc caa cag cat ctg agg 224
 Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln His Leu Arg

5

10

15

tat agc ttt ttg gga gta cct gct ttc ttg cct cct gga gga tat ttt 272
 Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly Gly Tyr Phe

20

25

30

35

ctg tcc tgg ggc ttc atg gcc cct ctc ttc cct gtt aca cat tgc tgt 320
 Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr His Cys Cys

40

45

50

gct tca gag cct ttg cag ctg cra cct agt tgaatccaca taggsttcc 370
 Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

55

60

tccacacggg gggaaggatc ttgctgcttt cactcacagg accagggagt tyttcaatca 430
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 acgcttggag tgggatgtgt gtgctactgg catctagtgg ctgctaaaca tctacactg 550
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<210> 124

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (59)

<223> unknown

<400> 124

Met Asp Leu Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln

1 5 10 15

His Leu Arg Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly

20 25 30

Gly Tyr Phe Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr

35 40 45

His Cys Cys Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

50 55 60

<210> 125

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (775).. (1017)

<220>

<221> unsure

<222> (200)

<223> g or a

<400> 125

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ttctccctga ctccagcagg gcaaggaatg taaccgagag gtgtgtggg ctgggctctg 180
 gtgccctctt ccttgcccr gaacacctct cctctgatt ccttggcac ctgtctttc 240
 tgtctgitta cctgtctccc tgcctgccc tctgcatctt ttgcagccc ccttgacttc 300
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 ccactgcaact ccagcctggg caacagagcg agactccgic ttaaaaaaaaa aaaaaaaaaag 660
 aacgcccttt tactgtctc atcatcccag tttagggcag tgctggagtg gggaaggccg 720
 tcttagacca tagaggcttg aagacgtga gagatcatcc agcccagccc ctig atg 777

Met

1

tta cag agc aga aga cag atg ccc aaa cag gag aag gca ctt gcc cac 825
 Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala His

5

10

15

ggt cat acg gca ggt tgc cac aaa acc aag atg gca gcc ctt cct cag 873
 Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro Gln

20

25

30

cgt gcc tca ctg cca ctc cca gag cca ggg agc ccc ata aaa ccc aca 921
 Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro Thr

35

40

45

tca tgt ctt aag agt ata tct ggc tcc ttg acc agc aat cgg ccc tgg 969
 Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro Trp

50

55

60

65

gag cca cca ggt ggg aaa agc gcc tct gcc aga gtc cag gcc ttg gga 1017

Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly

70

75

80

tgacagacag ctgccccga cactcgggcc ccactcaagg atgtagggcc ttttctggcc 1077

cctgaccctt ccttgggcat tgggagcgtg gggacggggc tggccttggg aggagcggca 1137

ggggcatcac ctctttctgc tgccttctcc tgcctctacc ctcaagggcc tgggggctgc 1197

ccagctgcct ctatgccctt ctgggggtct cagccactg ctgacacttc tgcaatccag 1257

agaaacacta aataaagcaa tacgtgtttg cc 1289

<210> 126

<211> 81

<212> PRT

<213> Homo sapiens

<400> 126

Met Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala

1

5

10

15

His Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro

20

25

30

Gln Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro

35

40

45

Thr Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro

50

55

60

Trp Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu

65

70

75

80

Gly

<210> 127

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (734).. (886)

<220>

<221> unsure

<222> (276)

<223> g or t

<400> 127

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ggaattacag gcacgcacca ccatgccctga ctaattttgt attttttagta gacatggggt 180
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aagttgatgg caattcttca catgtaaaca gtgccagtgc acagaacctt tatatatitt 360
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tcagctactt gggaggctga ggtgagagga tcacttgagc ttgggtgagg tgaggctgca 720
gtgagtcctg atc atg ctg ctg cac tca atc ttg gac aac aga gca aga 769

```

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg

1

5

10

ccc tgt ctg aaa aaa aaa aaa aat ata tat ata tat ata tat tat ttt 817

Pro Cys Leu Lys Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe

15

20

25

tat gag gtg aag tgc atc aaa ctt ggg aaa gat ttg agg agg ctg gga 865

Tyr Glu Val Lys Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly

30

35

40

acc tcc tgg aaa acc act cct tgaagaaaga tatgagagac atttagaagt 916

Thr Ser Trp Lys Thr Thr Pro

45

50

gattcctgct ttcagaagga ggtggattca aatacatcaa aagtcacctc ctctgctaag 976

tgittatagt tcaatgaata attcaatat ttgtatgtgt tcttgatcatt ttattttttt 1036

ctgaaaaact tccaaaaatt tgaaaaataaa attacagcct tttcttctt 1085

<210> 128

<211> 51

<212> PRT

<213> Homo sapiens

<400> 128

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg Pro Cys Leu Lys

1

5

10

15

Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe Tyr Glu Val Lys

20

25

30

Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly Thr Ser Trp Lys

35

40

45

Thr Thr Pro

50

<210> 129

<211> 1544

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1076)

<223> g or a

<400> 129

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acaaaaaccc aattttgttc atattgaagc atgaaataaa tgagagcaag gtagggccaa 180

attaactctt gtggacagtc cctaaaagtc cagttctaca ttgtgaaaa ttgtggtgcc 240

atgaattaag atggatgact ggaaaaaggt gtggagaaa gatttaaaga tgaggaagag 300

atatttttag tataatgaagt taaccagga ctgatattc ataattcagt gctgtggaaa 360

tgaaaaaaat gattgaagag gtggaacgga aatgacctta gggggaaaaa aaaggaccaa 420

agaagtciga ttaaaagttg aaatcagtat ttctgaattc aaattgcttg aatttccaaa 480

atagtcagta aaggaictaa tagaaccaga attatttggg tgaattctgc aggttttatg 540

ggcttgtcac aacgtgaagg gctggaatgt atattaccaa atgggaattt ccattgtagg 600

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tgttcccat tcatgtgttc tgaattcagc tcatctccca gcataatagat atatcctcct 720

ttaactccga ccagaacct tcttccgtg gcactccca cccatagacc ttcagatcat 780

ctcccacacc ctggatctca ctctctctt agtaacagag acactccga ggttggactt 840

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gcalcagttt tacttaccaa atggtttaga gtcataagat gacctatit tatataaaag 1020

ttatattata gaataaaatg ttcatagca tagactgta agataaaaaa ataggraatc 1080

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ctaaagatgc caggatattg gggctgaggg gagtttgagg tgtt 1544

<210> 130

<211> 508

<212> DNA

<213> Homo sapiens

<400> 130

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atgggaaaca ggttatcggg ggattcatga agtcagttag agtaattgct tcttttttgc 120

gggtgaactg aatgtatttc ttacacaaat ctgatgtta acaattaaaa agaagaaatg 180

acatgcaagt aggtctttagc agaaaaatgc aggcctgggca tgagtcatgt tgttaccctc 240

ccacatgctc ctacaatcca cagagatgcc tgtctgcagg ttcttgaagt tattgttagt 300

atttggtatc tcaaattttt cgtcactgtt cacatgccac ttctctctgtg cacagtggta 360

tectcatttg ctttttaacc tacactgagg agtccttgc aggttgcact gattttccaa 420

ttctgcagta atgagtaagc tcacggcatg gggaagaaga cagtcagtc aatgaagttc 480

tctaaattat tttaacattg ccttiigaa

508

<210> 131

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (50)

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<221> unsure

<222> (54)

<223> g or c

<220>

<221> unsure

<222> (300)

<223> g or c

<220>

<221> unsure

<222> (407)

<223> g or a

<220>

<221> unsure

<222> (415)

<223> a, c, g or t

<220>

<221> unsure

<222> (417)

<223> g or c

<220>

<221> unsure

<222> (419)

<223> t or c

<220>

<221> unsure

<222> (430)

<223> a or t

<220>

<221> unsure

<222> (448)

<223> t or c

<220>

<221> unsure

<222> (449)

<223> g or t

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<221> unsure

<222> (472)

<223> a, c, g or t

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gtggccaccc ttgggtcag acagctctgg gccttttgac cacaagccag cccctcgccc 180

tctctgtggc atagtctct ctagccccagg actgcagggc ggcttccctc aagcttcca 240

aggctcaaaa gaaatttggc tccatccaag aaggtccag ctcccctact ggccctggs 300

ttcaggccca caccctggg ccagggccag agagtgtgc tcaggagaat tcaatgggct 360

ctagagagac acacagaaag ttgggcatt tgggaaattt tcaaggrtgt atgintsgyt 420

cacgtatggw gcaggttgc ctggiccykg ggtgcaggga agtgggctgc anggaagtgg 480

attggagggg agcttgagga atataaggag cgggggtgga gactcaggct atggacaagg 540

acagcccaaa ggttgggaag acctggcctt agtcgtctc agcctagggg cagggcagtg 600

aagaaagctc tccccgtcc tgttgtaatg acccagagta gcctccccag gccggcatct 660

tatgtgtgc ttccaccatc ctcatgggtg cacttttcta ggctgtctc ccagcattgt 720

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<210> 132

<211> 508

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (223)

<223> a, c, g or t

<220>

<221> unsure

<222> (237)

<223> a, c, g or t

<220>

<221> unsure

<222> (380)

<223> a, c, g or t

<220>

<221> unsure

<222> (468)

<223> a, c, g or t

<400> 132

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gagattcttc catlittaga gctgagagag cacttgtgaa acacacacac atgcacaaac 180

atataaacat gcatacaggc atgcacatgc acacacaaat acncatacac acacacnagc 240

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tcttaggaat atgccaaagc ttttcaaagc ctctatggac agctcatlcc ttaacttttc 360

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508

<210> 133

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (313)

<223> a, c, g or t

<220>

<221> unsure

<222> (336)

<223> g or c

<220>

<221> unsure

<222> (401)

<223> g or c

<400> 133

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ccgc 484

<210> 134

<211> 605

<212> DNA

<213> Homo sapiens

<400> 134

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ggaatttgag ttctctctaa cccagcttac tglgggacat aggaaaactc agtagaaata 180
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caaattagtt cttttcccc cagaggggaa agttatgttc tgcaaatagt gtgtgtctta 360

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tataggaatc ctgtagtgcc actagttaaa tgccgaattc tcatctggat gttaccalca 480

aacatcagta cacttgteat ttacatgtg tttaatgtga cagtttttca gtactgtatg 540

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atccc 605

<210> 135

<211> 1786

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (151)

<220>

<221> unsure

<222> (689)

<223> g or a

<400> 135

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Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1

5

10

15

tac ctc tct cca cag cag ggc tct caa aac cat ttt gat ccc cca ttg 97

Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

20

25

30

gca gag ggt tcc cct ctt tac aga gtt cag tca tta aaa gca tgg atc 145

Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

35

40

45

agc tgt taatctcatt ggaggaggga actgtttcct gcattcattc atctgggaac 201

Ser Cys

50

cttcttgagt agccactgtc tgcagccac tgcctagag atgggaaaac agcacggaac 261

aaaaccaagg tcttcttcc agcgaattta tctcttcag gaagctgggt cctgccacca 321

acttagcagg caacagtct cctccctag tggcacagg gtaccagttt ttaggaaaa 381

gtgtccagc aaaggaagaa agcagaccaa cccagctgcc ttaccttatt ctggggccat 441

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gtcaagacc ctgggccctg ctgagcgtga aacaggaagg caatgggatg agttgtctgg 621

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tgatccagca gctgtccag gagaggcct cttttttt ccagccagc tgtgtctttg 801

catgagactc cttggggcct gggcacagag agaaaagaat tgagactcag gaggtcagt 861

gggtgagaaa atgcaaagtg gcttcacaga cacagggtg tgggagcaga tgcacgggga 921

acttgggaga tgaattcag ggccttcga cgccttgtct caggaacatg cttgagaaa 981

aatggtagca tctttccat aactcagct ccttcccta gtctccctga agtgtgact 1041

tttagtatct ggagctcagt gatcccatg aatgaggat aaagtttcac tcttggtatt 1101

ttctaactag tgctaggga agtctgaga cagatcaca gccactgctt ggcatagc 1161

gcctccacc aataagcaaa ctggagattc ctacgctct ctggacacc cacatctcat 1221

tcttctcaca gcagagaagc tctcccttca gccctgagctg tcttctttct gctgcagtgc 1281
 agcctgctcc ctectaccct ggcctcaagg aaggctggaa acatcttctg catttcaaag 1341
 tcttcacttt gacttatttg gccctcatct tggcatggaa ggtggcaggc agaatggaaa 1401
 tacctccccc caaacaaaac agatattctt gcgtgtgtaa gggcagaagg gacaagctct 1461
 ctatcccatg agactagggg ccggagccca cctgcccttc cccacaactt ttctgctca 1521
 aaccctctcc tcttgacaca ctggaatctg tattatatat attttaaga aaatacaatg 1581
 atggltgtct ggltttgttg tttttacagg tgttgtggaa taaaaactgt aagaaaatta 1641
 agtatttaaa atgttccaat aaagtggggc ttttgttat tctaataat tattgtgtac 1701
 ctattgtaaa tatgaaacac tcttattttg caagctgagg acacaatttg tactgttgtt 1761
 atatataaat aaagtttact gaatt 1786

<210> 136

<211> 50

<212> PRT

<213> Homo sapiens

<400> 136

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1	5	10	15
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Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

20	25	30
----	----	----

Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

35	40	45
----	----	----

Ser Cys

50

<210> 137

<211> 835

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (535).. (729)

<400> 137

gaaaaatctc attatttcaa aatgatagac atalaccaa aacaagtcta taatgtgagt 60
 agttactaaa atttacacat cttaaaagtg tgtaaatgct taaatttcag aattaccatc 120
 agaaccleaa ttgacatlec ttggaatagg ctaataagtg acaataaga ttaataagat 180
 tttlcaaaat cgccaggact ggtgaatata aatgatgatt gaactggaat aatattgggg 240
 accaaatcaa atgaatgatt aaattatgaa gctcatatcc ttttgaaggt agttgcaaag 300
 agacatttca aaactgccct aggccattgc agcatcctta gatgggacgc ataatcatta 360
 ccttaaagca tcaccactca tttigaccat atagatttta ttatgttagt ttaaaaggtc 420
 aatcagcctc atgactttat agttatgtct tgtattttaa aacatttttt atacatttgg 480
 ttatgttgat aaacaaaaaa catttgattt ataaaatata tatttgaata aatt atg 537

Met

1

agc tat cct ttc aaa cag cta ttg gca agt ttt aaa ccc aaa ata tat 585
 Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile Tyr

5

10

15

aca cat agt tct gta ata aaa ctg ttt gac ttc tca agt aac atg act 633
 Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met Thr

20

25

30

tcc tta ttt ctg aac agt act ggt tac ttt caa aat gaa ttt tta ttg 681
 Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu Leu

35

40

45

aga ttt tcc att aac tat ttt ttt caa aga ctg aaa ttt tgt acc aag 729

Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr Lys

50

55

60

65

taaatccagg ctttatglac aaacatgttg ttgttttat ttggggctgg gggaggtata 789

tgatgagcag acttcicgga attcataata aattttctaa aagcct

835

<210> 138

<211> 65

<212> PRT

<213> Homo sapiens

<400> 138

Met Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile

1

5

10

15

Tyr Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met

20

25

30

Thr Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu

35

40

45

Leu Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr

50

55

60

Lys

65

<210> 139

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (201)

<220>

<221> unsure

<222> (348)

<223> t or c

<220>

<221> unsure

<222> (353)

<223> a or t

<220>

<221> unsure

<222> (358)

<223> a or t

<220>

<221> unsure

<222> (363)

<223> a or t

<220>

<221> unsure

<222> (368)

<223> g or a

<400> 139

tgt ttc agt gtg act gtc ttg tta gag gtg aag ttt atc cag ggt aac 48

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1

5

10

15

ttg ctc act aac tat tcc ttt tta tgg cct ggg gtt aaa ggg agc atg 96

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met
 20 25 30
 gct cac act ggt gaa aat aag gaa ggc ctg gtc tta tct tgt att aat 144
 Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn
 35 40 45
 aat act ggc tgc att cca cca gcc aga gat ttc tat ctg cga aga cct 192
 Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro
 50 55 60
 atg aaa cac tgaagagaaa tgtaggcaga aggaaatggc cacatatcac 241
 Met Lys His
 65
 aagttctatt atatatcttt ttgtaaatac atattgtata ttacttggat gttttcttat 301
 atcatttact gtcttttga gttaagtca gtttttactc tctcaaytta cwatgtwaca 361
 twglaartaa cataatgtcc ttattatatt atatttaagc atctaacata tagagttgtt 421
 ttcataataag tttaagataa atgtcaaaaa tatatgttct ttgtttttc ttgtctttaa 481
 aattatgtat cttttcccttt tctttttttt aagaataatt tattgttcag gagaaagaat 541
 glatatgtaa ctgaaactat ctgaagaatg cacattgaag gccgtgaggt actgataaac 601
 taaagaattt attattcaaa atact 626

<210> 140

<211> 67

<212> PRT

<213> Homo sapiens

<400> 140

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn
 1 5 10 15
 Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

20 25 30
Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn

35 40 45
Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro

50 55 60
Met Lys His

65

<210> 141

<211> 525

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103).. (525)

<400> 141

aagaaatgga ggactcagaa ccaaggattt ccaagtgatt tcitccaaag cacaggaatc 60
tcactctgtt aaagctggtc tgttctaact gagatgacag tc atg tcc ctt tcc 114

Met Ser Leu Ser

1

agg gac ctc aag gac gac ttt cac agt gac acg gla ctc tcc atc tta 162

Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val Leu Ser Ile Leu

5 10 15 20

aat gag cag cgc att cgg ggc att tta tgc gat gtc act atc att gtg 210

Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val Thr Ile Ile Val

25 30 35

gaa gat acc aaa ttt aaa gcc cat agc aat gtt ctg gca gct tca agc 258

Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu Ala Ala Ser Ser

40

45

50

ctg tal ttt aaa aat atc ttt tgg agc cat aca atc tgt att tcc agc 306

Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile Cys Ile Ser Ser

55

60

65

cac gtc ctg gag ctg gac gat ctc aaa gct gaa gtg ttt act gaa ata 354

His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val Phe Thr Glu Ile

70

75

80

ctt aat tat atc tac agt tcc aca gtc gtt gtc aag aga cag gaa aca 402

Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys Arg Gln Glu Thr

85

90

95

100

gtc act gat ctc gca gct gca gga aaa aag ctg gga ata tgc ttc ttg 450

Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly Ile Ser Phe Leu

105

110

115

gaa gac ctt act gat cgc aac ttc tca aat tcc ccg ggt ccc tat gla 498

Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro Gly Pro Tyr Val

120

125

130

ttc tgt att act gaa aag gga gtg gtt 525

Phe Cys Ile Thr Glu Lys Gly Val Val

135

140

<210> 142

<211> 141

<212> PRT

<213> Homo sapiens

<400> 142

Met Ser Leu Ser Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val

1	5	10	15
Leu Ser Ile Leu Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val			
20	25	30	
Thr Ile Ile Val Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu			
35	40	45	
Ala Ala Ser Ser Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile			
50	55	60	
Cys Ile Ser Ser His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val			
65	70	75	80
Phe Thr Glu Ile Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys			
85	90	95	
Arg Gln Glu Thr Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly			
100	105	110	
Ile Ser Phe Leu Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro			
115	120	125	
Gly Pro Tyr Val Phe Cys Ile Thr Glu Lys Gly Val Val			
130	135	140	

<210> 143

<211> 1827

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138).. (1307)

<400> 143

gagacttggg ctggagccgc cctgggtgtc agcggctcgg ctcccgcgca cgctccggcc 60

gtcgcgcagc ctccggcacct gcaggctccgt gcgtcccgcg gctggcgccc ctgactccgt 120
 cccggccagg gagggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac 170
 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn
 1 5 10
 ttg ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc tgc 218
 Leu Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser
 15 20 25
 cgg gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg 266
 Arg Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val
 30 35 40
 gag gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag 314
 Glu Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu
 45 50 55
 gtg tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc 362
 Val Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe
 60 65 70 75
 aaa cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc 410
 Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val
 80 85 90
 aca aca agc aaa cct gga gta tcc ttg gtc tac tcc atg ccc tcc cgg 458
 Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg
 95 100 105
 aac ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc 506
 Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro
 110 115 120
 tac agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc 554
 Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly

125	130	135	
cac agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct	602		
His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro			
140	145	150	155
cca tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc	650		
Pro Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr			
160	165	170	
ctg agc tgc cag tct cca agg agt aag cct gct gtc caa tac cag tgg	698		
Leu Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp			
175	180	185	
gat cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat	746		
Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp			
190	195	200	
gtc atc cgt ggg tct tta agc ctc acc aac ctt tgc tct tcc atg gct	794		
Val Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala			
205	210	215	
gga gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt	842		
Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys			
220	225	230	235
aat gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct	890		
Asn Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala			
240	245	250	
gga gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg	938		
Gly Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu			
255	260	265	
gtc ctc ttg tac cac cgc cgg ggc aag gcc ctg gag gag cca gcc aat	986		

Val Leu Leu Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn

270

275

280

gat atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag 1034

Asp Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys

285

290

295

agc tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc 1082

Ser Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser

300

305

310

315

gca cga gcc ctc tgg cca ccc cat ggc cct ccc agg cct ggt gca ttg 1130

Ala Arg Ala Leu Trp Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu

320

325

330

acc ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg 1178

Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu

335

340

345

ccc acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt 1226

Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly

350

355

360

ggg gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct glg atg 1274

Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met

365

370

375

gtg cct gcc cag agt caa gct ggc tct ctg gta tgatgacccc accactcatt 1327

Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val

380

385

390

ggctaaagga tttaggggtct ctcttctcta taagggtcac ctctagcaca gaggcctgag 1387

tcatgggaaa gagtcacact cctgacctt agtactctgc cccacctct cttactgtg 1447

ggaaaaccat ctcaagtaaga cctaagtgc caggagacag aaggagaaga ggaagtggat 1507

ciggaattgg gaggagcctc caccacccc tgactctctc ttatgaagcc agctgctgaa 1567

attagctact caccaagagi gaggggcaga gacttccagt cactgagtct cccaggcccc 1627
 cttgatctgt accccacccc tatctaacac cacccttggc tcccactcca gctccctgta 1687
 ttgalataac ctgtcaggct ggcttggta gglttactg gggcagagga tagggaatct 1747
 cttattaaaa ctaacaigaa atatgtgttg ttttcatttg caaatltaaa taaagataca 1807
 taatgtttgt atgagataag 1827

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1 5 10 15

Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln

20 25 30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val

35 40 45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln

50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys

65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg

100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val

115 120 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
 130 135 140
 Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
 145 150 155 160
 Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
 165 170 175
 Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
 180 185 190
 Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
 195 200 205
 Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
 210 215 220
 Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
 225 230 235 240
 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
 245 250 255
 Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
 260 265 270
 Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
 275 280 285
 Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300
 Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Trp
 305 310 315 320
 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly

340

345

350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

355

360

365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser

370

375

380

Gln Ala Gly Ser Leu Val

385

390

<210> 145

<211> 3466

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84).. (2726)

<400> 145

tgcgggaagc gatgtagtag ctgccaggct gtcccccgcc ctgcccggcc cgagccccgc 60

gggccgccgc cgccaccgcc gcc atg aag aag cag ttc aac cgc atg aag cag 113

Met Lys Lys Gln Phe Asn Arg Met Lys Gln

1

5

10

ctg gct aac cag acc gtg ggc aga gct gag aaa aca gaa gtc ctt agt 161

Leu Ala Asn Gln Thr Val Gly Arg Ala Glu Lys Thr Glu Val Leu Ser

15

20

25

gaa gat cta tta cag att gag aga cgc ctg gac acg gtg cgg tca ata 209

Glu Asp Leu Leu Gln Ile Glu Arg Arg Leu Asp Thr Val Arg Ser Ile

30

35

40

tgc cac cat tcc cat aag cgc ttg gtg gca tgt ttc cag ggc cag cat	257
Cys His His Ser His Lys Arg Leu Val Ala Cys Phe Gln Gly Gln His	
45 50 55	
ggc acc gat gcc gag agg aga cac aaa aaa ctg cct ctg aca gct ctt	305
Gly Thr Asp Ala Glu Arg Arg His Lys Lys Leu Pro Leu Thr Ala Leu	
60 65 70	
gct caa aat atg caa gaa gca tgc act cag ctg gaa gac tct ctc ctg	353
Ala Gln Asn Met Gln Glu Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu	
75 80 85 90	
ggg aag atg ctg gag acg tgt gga gat gct gag aat cag ctg gct ctc	401
Gly Lys Met Leu Glu Thr Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu	
95 100 105	
gag ctc tcc cag cac gaa gtc ttt gtt gag aag gag atc gig gac cct	449
Glu Leu Ser Gln His Glu Val Phe Val Glu Lys Glu Ile Val Asp Pro	
110 115 120	
ctg tac ggc ata gct gag gtg gag att ccc aac atc cag aag cag agg	497
Leu Tyr Gly Ile Ala Glu Val Glu Ile Pro Asn Ile Gln Lys Gln Arg	
125 130 135	
aag cag ctt gca aga ttg gtg tta gac tgg gat tca gtc aga gcc agg	545
Lys Gln Leu Ala Arg Leu Val Leu Asp Trp Asp Ser Val Arg Ala Arg	
140 145 150	
tgg aac caa gct cac aaa tcc tca gga acc aac ttt cag ggg ctt cca	593
Trp Asn Gln Ala His Lys Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro	
155 160 165 170	
tca aaa ata gat act cta aag gaa gag atg gat gaa gct gga aat aaa	641
Ser Lys Ile Asp Thr Leu Lys Glu Glu Met Asp Glu Ala Gly Asn Lys	
175 180 185	

gta gaa cag tgc aag gat caa ctt gca gca gac atg tac aac ttt atg 689
 Val Glu Gln Cys Lys Asp Gln Leu Ala Ala Asp Met Tyr Asn Phe Met
 190 195 200
 gcc aaa gaa ggg gag tat ggc aaa ttc ttt gtt acg tta tta gaa gcc 737
 Ala Lys Glu Gly Glu Tyr Gly Lys Phe Phe Val Thr Leu Leu Glu Ala
 205 210 215
 caa gca gat tac cat aga aaa gca tta gca gtc tta gaa aag acc ctc 785
 Gln Ala Asp Tyr His Arg Lys Ala Leu Ala Val Leu Glu Lys Thr Leu
 220 225 230
 ccc gaa atg cga gcc cat caa gat aag tgg gcg gaa aaa cca gcc ttt 833
 Pro Glu Met Arg Ala His Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe
 235 240 245 250
 ggg act ccc cta gaa gaa cac ctg aag agg agc ggg cgc gag att gcg 881
 Gly Thr Pro Leu Glu Glu His Leu Lys Arg Ser Gly Arg Glu Ile Ala
 255 260 265
 ctg ccc att gaa gcc tgt gtc atg ctg ctt ctg gag aca ggc atg aag 929
 Leu Pro Ile Glu Ala Cys Val Met Leu Leu Leu Glu Thr Gly Met Lys
 270 275 280
 gag gag ggc ctt ttc cga att ggg gct ggg gcc tcc aag tta aag aag 977
 Glu Glu Gly Leu Phe Arg Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys
 285 290 295
 ctg aaa gct gct ttg gac tgt tct act tct cac ctg gat gag ttc tat 1025
 Leu Lys Ala Ala Leu Asp Cys Ser Thr Ser His Leu Asp Glu Phe Tyr
 300 305 310
 tca gac ccc cat gct gta gca ggt gct tta aaa tcc tat tta cgg gaa 1073
 Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu

315	320	325	330	
ttg cct gaa cct ttg atg act ttt aat ctg tat gaa gaa tgg aca caa	1121			
Leu Pro Glu Pro Leu Met Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln				
	335	340	345	
gtt gca agt gtg cag gat caa gac aaa aaa ctt caa gac ttg tgg aga	1169			
Val Ala Ser Val Gln Asp Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg				
	350	355	360	
aca tgt cag aag ttg cca cca caa aat ttt gtt aac ttt aga tat ttg	1217			
Thr Cys Gln Lys Leu Pro Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu				
	365	370	375	
atc aag ttc ctt gca aag ctt gct cag acc agc gat gtg aat aaa atg	1265			
Ile Lys Phe Leu Ala Lys Leu Ala Gln Thr Ser Asp Val Asn Lys Met				
	380	385	390	
act ccc agc aac att gcg att gtg tta ggc cct aac ttg tta tgg gcc	1313			
Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Ala				
395	400	405	410	
aga aat gaa gga aca ctt gct gaa atg gca gca gcc aca tcc gtc cat	1361			
Arg Asn Glu Gly Thr Leu Ala Glu Met Ala Ala Ala Thr Ser Val His				
	415	420	425	
gtg gtt gca gtg att gaa ccc atc att cag cat gcc gac tgg ttc ttc	1409			
Val Val Ala Val Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe				
	430	435	440	
cct gaa gag glg gaa ttt aat gta tca gaa gca ttt gta cct ctc acc	1457			
Pro Glu Glu Val Glu Phe Asn Val Ser Glu Ala Phe Val Pro Leu Thr				
	445	450	455	
acc ccg agt tct aat cac tca ttc cac act gga aac gac tct gac tcg	1505			
Thr Pro Ser Ser Asn His Ser Phe His Thr Gly Asn Asp Ser Asp Ser				

460	465	470	
ggg acc ctg gag agg aag cgg cct gct agc atg gcg gtg atg gaa gga	1553		
Gly Thr Leu Glu Arg Lys Arg Pro Ala Ser Met Ala Val Met Glu Gly			
475	480	485	490
gac ttg gtg aag aag gaa agc ttt ggt gtg aag ctt atg gac ttc cag	1601		
Asp Leu Val Lys Lys Glu Ser Phe Gly Val Lys Leu Met Asp Phe Gln			
	495	500	505
gcc cac cgg cgg ggt ggc act cta aat aga aag cac ata tcc ccc gct	1649		
Ala His Arg Arg Gly Gly Thr Leu Asn Arg Lys His Ile Ser Pro Ala			
	510	515	520
ttc cag ccg cca ctt ccg ccc aca gat ggc agc acc gtg gtg ccc gct	1697		
Phe Gln Pro Pro Leu Pro Pro Thr Asp Gly Ser Thr Val Val Pro Ala			
	525	530	535
ggc cca gag ccc cct ccc cag agc tct agg gct gaa agc agc tct ggg	1745		
Gly Pro Glu Pro Pro Pro Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly			
	540	545	550
ggt ggg act gtc ccc tct tcc gcg ggc ata ctg gag cag ggg ccg agc	1793		
Gly Gly Thr Val Pro Ser Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser			
555	560	565	570
cca ggc gac ggc agt cct ccc aaa ccg aag gac cct gta tct gca gct	1841		
Pro Gly Asp Gly Ser Pro Pro Lys Pro Lys Asp Pro Val Ser Ala Ala			
	575	580	585
gtg cca gca cca ggg aga aac aac agt cag ata gca tct ggc caa aat	1889		
Val Pro Ala Pro Gly Arg Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn			
	590	595	600
cag ccc cag gca gct gct ggc tcc cac cag ctc tcc atg ggc caa cct	1937		

Gln Pro Gln Ala Ala Ala Gly Ser His Gln Leu Ser Met Gly Gln Pro
 605 610 615
 cac aat gct gca ggg ccc agc ccg cat aca ctg cgc cga gct gtt aaa 1985
 His Asn Ala Ala Gly Pro Ser Pro His Thr Leu Arg Arg Ala Val Lys
 620 625 630
 aaa ccc gct cca gca ccc ccg aaa ccg ggc aac cca cct cct ggc cac 2033
 Lys Pro Ala Pro Ala Pro Pro Lys Pro Gly Asn Pro Pro Pro Gly His
 635 640 645 650
 ccc ggg ggc cag agt tct tca gga aca tct cag cat cca ccc agt ctg 2081
 Pro Gly Gly Gln Ser Ser Ser Gly Thr Ser Gln His Pro Pro Ser Leu
 655 660 665
 tca cca aag cca ccc acc cga agc ccc tct cct ccc acc cag cac acg 2129
 Ser Pro Lys Pro Pro Thr Arg Ser Pro Ser Pro Pro Thr Gln His Thr
 670 675 680
 ggc cag cct cca ggc cag ccc tcc gcc ccc tcc cag ctc tca gca ccc 2177
 Gly Gln Pro Pro Gly Gln Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro
 685 690 695
 cgg agg tac tcc agc agc ttg tct cca atc caa gct ccc aat cac cca 2225
 Arg Arg Tyr Ser Ser Ser Leu Ser Pro Ile Gln Ala Pro Asn His Pro
 700 705 710
 ccg ccg cag ccc cct acg cag gcc acg cca ctg atg cac acc aaa ccc 2273
 Pro Pro Gln Pro Pro Thr Gln Ala Thr Pro Leu Met His Thr Lys Pro
 715 720 725 730
 aat agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga 2321
 Asn Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly
 735 740 745
 ctt gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt 2369

Leu Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser
 750 755 760
 act ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc 2417
 Thr Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr
 765 770 775
 ctg gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta 2465
 Leu Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu
 780 785 790
 ccg aga ccg aga cca gla cca aag cca agg aac cgg ccc agc gtg ccc 2513
 Pro Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro
 795 800 805 810
 cca ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc ctc 2561
 Pro Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu
 815 820 825
 acc aac aca gca cca aca gct tcc aag ata gta aca gac tcc aat tcc 2609
 Thr Asn Thr Ala Pro Thr Ala Ser Lys Ile Val Thr Asp Ser Asn Ser
 830 835 840
 agg gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac 2657
 Arg Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp
 845 850 855
 tca gcc agc aaa gac gtg cct ggc cgc atc ctg ctg gat ata gac aat 2705
 Ser Ala Ser Lys Asp Val Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn
 860 865 870
 gat acc gag agc act gcc ctg tgaagaaagc cctttcccag ccctccacca 2756
 Asp Thr Glu Ser Thr Ala Leu
 875 880

cticcacccct ggcgagtggga gcaggggcag gcgaacctct tictttgcag accgaacagt 2816
 gaaaagcttt cagtgaggga caaaggaggg cctcactgtg cgggacctgg ccttcigcac 2876
 ggcccaagga gaacctggag gccaccacta aagctgaatg acctgtgtct tgaagaagtt 2936
 ggctttcttt acatgggaag gaaatcatgc caaaaaaatc caaaacaaag aagtaacctgg 2996
 agtggagaga glattcctgc tgaaacgcgc ataggaagct ttgttcctg ctgttaatgc 3056
 gggcagcacc tacagcaact tggaatgagt aagaagcagt gcgttaacta tctatttaat 3116
 aaaatgcgct cattatgcaa gtcgcctact ctcigtacc tggacgttca ttcttatgta 3176
 ttaggagggga ggctgcgctc cticagactt gctgcagaat cattttgtat caigtatggt 3236
 ctgtgtctcc ccagtcacct cagaacctg cccatggatg gtgactgcig gcctgtgcac 3296
 ctcatcaaac tggatgigac ccatgccgcc tcgttggatt gtcggaatgt agacagaaat 3356
 glactgttct ttttttttt tttaaacaat gtaattgcta ctgataagg accgaacatt 3416
 attctagttt catgtttaat ttgaattaaa tataattctgt ggtttatatg 3466

<210> 146

<211> 881

<212> PRT

<213> Homo sapiens

<400> 146

Met Lys Lys Gln Phe Asn Arg Met Lys Gln Leu Ala Asn Gln Thr Val

1 5 10 15

Gly Arg Ala Glu Lys Thr Glu Val Leu Ser Glu Asp Leu Leu Gln Ile

20 25 30

Glu Arg Arg Leu Asp Thr Val Arg Ser Ile Cys His His Ser His Lys

35 40 45

Arg Leu Val Ala Cys Phe Gln Gly Gln His Gly Thr Asp Ala Glu Arg

50 55 60

Arg His Lys Lys Leu Pro Leu Thr Ala Leu Ala Gln Asn Met Gln Glu

65	70	75	80
Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu Gly Lys Met Leu Glu Thr			
	85	90	95
Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu Glu Leu Ser Gln His Glu			
	100	105	110
Val Phe Val Glu Lys Glu Ile Val Asp Pro Leu Tyr Gly Ile Ala Glu			
	115	120	125
Val Glu Ile Pro Asn Ile Gln Lys Gln Arg Lys Gln Leu Ala Arg Leu			
	130	135	140
Val Leu Asp Trp Asp Ser Val Arg Ala Arg Trp Asn Gln Ala His Lys			
145	150	155	160
Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro Ser Lys Ile Asp Thr Leu			
	165	170	175
Lys Glu Glu Met Asp Glu Ala Gly Asn Lys Val Glu Gln Cys Lys Asp			
	180	185	190
Gln Leu Ala Ala Asp Met Tyr Asn Phe Met Ala Lys Glu Gly Glu Tyr			
	195	200	205
Gly Lys Phe Phe Val Thr Leu Leu Glu Ala Gln Ala Asp Tyr His Arg			
	210	215	220
Lys Ala Leu Ala Val Leu Glu Lys Thr Leu Pro Glu Met Arg Ala His			
225	230	235	240
Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe Gly Thr Pro Leu Glu Glu			
	245	250	255
His Leu Lys Arg Ser Gly Arg Glu Ile Ala Leu Pro Ile Glu Ala Cys			
	260	265	270
Val Met Leu Leu Leu Glu Thr Gly Met Lys Glu Glu Gly Leu Phe Arg			
	275	280	285

Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys Leu Lys Ala Ala Leu Asp
 290 295 300
 Cys Ser Thr Ser His Leu Asp Glu Phe Tyr Ser Asp Pro His Ala Val
 305 310 315 320
 Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro Leu Met
 325 330 335
 Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln Val Ala Ser Val Gln Asp
 340 345 350
 Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg Thr Cys Gln Lys Leu Pro
 355 360 365
 Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu Ile Lys Phe Leu Ala Lys
 370 375 380
 Leu Ala Gln Thr Ser Asp Val Asn Lys Met Thr Pro Ser Asn Ile Ala
 385 390 395 400
 Ile Val Leu Gly Pro Asn Leu Leu Trp Ala Arg Asn Glu Gly Thr Leu
 405 410 415
 Ala Glu Met Ala Ala Ala Thr Ser Val His Val Val Ala Val Ile Glu
 420 425 430
 Pro Ile Ile Gln His Ala Asp Trp Phe Phe Pro Glu Glu Val Glu Phe
 435 440 445
 Asn Val Ser Glu Ala Phe Val Pro Leu Thr Thr Pro Ser Ser Asn His
 450 455 460
 Ser Phe His Thr Gly Asn Asp Ser Asp Ser Gly Thr Leu Glu Arg Lys
 465 470 475 480
 Arg Pro Ala Ser Met Ala Val Met Glu Gly Asp Leu Val Lys Lys Glu
 485 490 495

Ser Phe Gly Val Lys Leu Met Asp Phe Gln Ala His Arg Arg Gly Gly
 500 505 510
 Thr Leu Asn Arg Lys His Ile Ser Pro Ala Phe Gln Pro Pro Leu Pro
 515 520 525
 Pro Thr Asp Gly Ser Thr Val Val Pro Ala Gly Pro Glu Pro Pro Pro
 530 535 540
 Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly Gly Gly Thr Val Pro Ser
 545 550 555 560
 Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser Pro Gly Asp Gly Ser Pro
 565 570 575
 Pro Lys Pro Lys Asp Pro Val Ser Ala Ala Val Pro Ala Pro Gly Arg
 580 585 590
 Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn Gln Pro Gln Ala Ala Ala
 595 600 605
 Gly Ser His Gln Leu Ser Met Gly Gln Pro His Asn Ala Ala Gly Pro
 610 615 620
 Ser Pro His Thr Leu Arg Arg Ala Val Lys Lys Pro Ala Pro Ala Pro
 625 630 635 640
 Pro Lys Pro Gly Asn Pro Pro Pro Gly His Pro Gly Gly Gln Ser Ser
 645 650 655
 Ser Gly Thr Ser Gln His Pro Pro Ser Leu Ser Pro Lys Pro Pro Thr
 660 665 670
 Arg Ser Pro Ser Pro Pro Thr Gln His Thr Gly Gln Pro Pro Gly Gln
 675 680 685
 Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro Arg Arg Tyr Ser Ser Ser
 690 695 700
 Leu Ser Pro Ile Gln Ala Pro Asn His Pro Pro Pro Gln Pro Pro Thr

705 710 715 720
 Gln Ala Thr Pro Leu Met His Thr Lys Pro Asn Ser Gln Gly Pro Pro
 725 730 735
 Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu Glu Gln Pro Ser His
 740 745 750
 Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr Pro Pro Leu Gly Lys
 755 760 765
 Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu Ala Gly Gly Asn Pro
 770 775 780
 Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro Arg Pro Arg Pro Val
 785 790 795 800
 Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro Pro Pro Gln Pro Pro
 805 810 815
 Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr Asn Thr Ala Pro Thr
 820 825 830
 Ala Ser Lys Ile Val Thr Asp Ser Asn Ser Arg Val Ser Glu Pro His
 835 840 845
 Arg Ser Ile Phe Pro Glu Met His Ser Asp Ser Ala Ser Lys Asp Val
 850 855 860
 Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn Asp Thr Glu Ser Thr Ala
 865 870 875 880
 Leu

<210> 147

<211> 3021

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (140).. (1105)

<400> 147

gagctgccgc tctctctctt gcttcagccg cagtcgccac tggctgccctg aggtgctctt 60
 acagccctgtt ccaagtgtgg cttaatccgt ctccaccacc agatctttct cctgtggattc 120
 ctctgctaag accgctgcc atg cca gtg acg gla acc cgc acc acc atc aca 172

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr

1

5

10

acc acc acg acg tca tct tct ggc ctg ggg tcc ccc atg atc gtg ggg 220

Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly

15

20

25

tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag 268

Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln

30

35

40

ctg gtg tct acc tgc gtg gcc ttc tct ctg gtg gct agc gtg ggc gcc 316

Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala

45

50

55

tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc 364

Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys

60

65

70

75

ttc tcc gtg acc ctg atc atc ctc atc gtg gag ctg tgc ggg ctc cag 412

Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln

80

85

90

gcc cgc ttc ccc ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc 460

Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys

95	100	105	
tat gcg ggc ctc ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc			508
Tyr Ala Gly Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr			
110	115	120	
tat gtc cag ttc ctg tcc cac ggc cgt tcg cgg gac cac gcc atc gcc			556
Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala			
125	130	135	
gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg			604
Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val			
140	145	150	155
gcc tgg acc cgg gcc cgg ccc ggc gag atc act ggc tat atg gcc acc			652
Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr			
160	165	170	
gta ccc ggg ctg ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc			700
Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile			
175	180	185	
ttc gcg ttc atc agc gac ccc aac ctg tac cag cac cag ccg gcc ctg			748
Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu			
190	195	200	
gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc			796
Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile			
205	210	215	
gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc			844
Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro			
220	225	230	235
ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat			892
Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr			

240 245 250
 gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat 940
 Ala Thr Ala Leu Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr
 255 260 265
 ggc ggc cag cct cgg cgc tgg aga gat gta agc tgc agc cgc agc cat 988
 Gly Gly Gln Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His
 270 275 280
 gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg 1036
 Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu
 285 290 295
 acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc 1084
 Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
 300 305 310 315
 cac ctg gtt ttt gtc aag gtc taagactctc ccaagaggct cccgttccct 1135
 His Leu Val Phe Val Lys Val
 320
 ctccaaccctc ttgtttcttc ttgcccagagt ttcttttatg gactacttct ttctctcgcc 1195
 ttctctctgt ttctctcttc ctgtctcccc tcccctccac ctttttcttt ccttcccatt 1255
 tccctgcact ctaaccagtt ctggatgca tcttcttctt tccccttctt ctgctgtttt 1315
 ccttctctgt ttgttttgtt gccacatcc tgttttcacc cctgagctgt ttctcttttt 1375
 ctttctcttc ttttttttt tttttaaga cggattctca ctctgtggcc caggctggag 1435
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 acatatatat atatatatit ggaggtcagt aatttccaat gggcgggagg cattaagcac 1975
 cgacctggg tccclaggcc cggcctggca ctacgcttg ccagagattg gctccagaat 2035
 ttttgccagg ctacagAAC acccactgcc tagaggccat cttaaaggaa gcaggggctg 2095
 gatgcctttc atcccaacta ttctctgttg tatgaaaaag aaaaaaaaaa aaaaagaagg 2155
 agtcggggcc gggcgtgggt gctcacgect glaatcccag cactilggga gaccaagtcA 2215
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 ctattaaaaa taaaaaatt agccgggcgt ggtggcgggc gcctglaatc ccaggtatit 2335
 ggggggactg agacaggaga atcccttcaa cccgggaggt ggaggttgca glaagtcAag 2395
 atggcaccac tggctccag cctgggggac agagcgagac tccatctcaa aaaaaaagg 2455
 gaatcggacg aagaaccaca ggatgttgaa gacaactgtc tgaaglatit gtgagggaca 2515
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 ttcttgcca ttaggacaaa aattactgag tggcccttaa agagggaagt ttgtttcag 2695
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 gctttgcttg aatgtgtagt gcacacgcac ggggtgtttct gtgtgctagt tgcctcttgc 2815
 tgcctcttcc tgcctgtctg ggactacat acataacgtg atatatatat atatatataa 2875
 atgtataaat atatatitit tttttttit aatccttgga gcttctgggt cctatcagtt 2935
 cctgttgita atcgtagaac cgttgctcct tccccattc ccgtatccat catgttcttt 2995
 ttctttttaa tatcaatata aaaggt 3021

<210> 148

<211> 322

<212> PRT

<213> Homo sapiens

<400> 148

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr Ser

1 5 10 15

Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala Leu

20 25 30

Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys

35 40 45

Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met

50 55 60

Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu

65 70 75 80

Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu

85 90 95

Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Gly Leu Phe

100 105 110

Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu

115 120 125

Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser

130 135 140

Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala

145 150 155 160

Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu

165 170 175

Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser

180 185 190

Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala

195 200 205

Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn
 210 215 220
 Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
 225 230 235 240
 Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val
 245 250 255
 Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg
 260 265 270
 Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys
 275 280 285
 Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu
 290 295 300
 Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val
 305 310 315 320
 Lys Val

<210> 149

<211> 4409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (39).. (2027)

<400> 149

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Met Ser Trp Leu Ser Ser

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5

tcc cag gga gtg gta cta aca gcc tac cac ccc agc ggc aag gac cag 104
 Ser Gln Gly Val Val Leu Thr Ala Tyr His Pro Ser Gly Lys Asp Gln
 10 15 20
 gcc gtc ggg aac agc cat gca aag gca ggg gag gaa gcc acc tcg agt 152
 Ala Val Gly Asn Ser His Ala Lys Ala Gly Glu Glu Ala Thr Ser Ser
 25 30 35
 cgc aga tat ggc cag tac act atg aac cag gaa agc acc acc atc aaa 200
 Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln Glu Ser Thr Thr Ile Lys
 40 45 50
 gtt atg gag aag cct cca ttt gat cga tca att tcc cag gat tct ttg 248
 Val Met Glu Lys Pro Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu
 55 60 65 70
 gat gaa cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc aag 296
 Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys
 75 80 85
 aaa tct agt gaa aac agc caa gaa gat caa gag gtg gtt gtt gtc aaa 344
 Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys
 90 95 100
 gag cct gat gag gga gaa ttg gaa gaa gag tgg ctt aaa gag gcc ggt 392
 Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu Trp Leu Lys Glu Ala Gly
 105 110 115
 tta tcc aat ctc ttc gga gag tct gct gga gat cca cag gaa agc att 440
 Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile
 120 125 130
 gtg ttt tta tca aca ttg acg cgg acc cag gca gca gca gtt cag aag 488
 Val Phe Leu Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys

135	140	145	150	
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac aaa cag tac				536
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn Lys Gln Tyr				
	155	160	165	
cag att cct gac gtc aga gac ata ttt gct caa cag aga gaa tca aaa				584
Gln Ile Pro Asp Val Arg Asp Ile Phe Ala Gln Gln Arg Glu Ser Lys				
	170	175	180	
gaa aca gct cca ggt ggc act gaa tgc cag tca ctt aga aca aat gaa				632
Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln Ser Leu Arg Thr Asn Glu				
	185	190	195	
aac aaa tac caa gga aga gat gac gag gca tct aac ctt gtt ggt gaa				680
Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu				
	200	205	210	
gag aag ctg atc cca cct gag gag acg cct gcc cct gaa aca gac atc				728
Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr Asp Ile				
	215	220	225	230
aac ctg gag gta tca ttt gcc gag caa gca ctc aat cag aaa gag agc				776
Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu Asn Gln Lys Glu Ser				
	235	240	245	
tcc aag gag aaa atc cag aag agc aaa ggc gat gat gcc aca tta cct				824
Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly Asp Asp Ala Thr Leu Pro				
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agt ttc aga ttg cca aaa gac aaa acg ggt acc aca agg att ggt gac				872
Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp				
	265	270	275	
ctc gca ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att gag				920
Leu Ala Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile Glu				

280	285	290	
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Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu Lys Gln Gln Lys			
295	300	305	310
gct gtg aaa atc aaa aca aaa gat tct ggt ctt ttt tgc gtt cca ttg	1016		
Ala Val Lys Ile Lys Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu			
315	320	325	
aca gcg cta tta gaa caa gat cag agg aaa gta cca gga atg cga ata	1064		
Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys Val Pro Gly Met Arg Ile			
330	335	340	
ccc ttg atc ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg	1112		
Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu			
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gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att aga atc aag	1160		
Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys			
360	365	370	
aat ctt tgc caa gaa cta gaa gca aag ttt tat gaa ggg act ttt aat	1208		
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375	380	385	390
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Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu Gln Ala

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Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp Ala Asn Arg Asp Thr Leu

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aag gcc ctt ctt gaa ttt ctc caa aga gta ata gat aat aaa gaa aaa 1448

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caa aaa ctt ctg tgg aca att ccc aag ttt att gta aac caa gtg agg 1640

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aag agt aca aat gat gct gac gtt cct cag gga gtg att cga gtg caa 1784

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Ala Pro His Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu

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cta aaa gcc agt gat gta ctt gcc agg ttt ctc agc caa gaa agt ggg 1880

Leu Lys Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly

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ggt gcc cag act ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga 1928

Val Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly

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625

630

gga aat att ggg gaa cgc tgc ctt gat gat gac act tac atg aag gat 1976

Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys Asp

635

640

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tta tat cag ctt aac cca aat gct gag tgg gtt ata aag tca aag cca 2024

Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser Lys Pro

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35 40 45

Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe Asp Arg Ser

50 55 60

Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile

65 70 75 80

Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln

85 90 95

Glu Val Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu

100 105 110

Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly

115 120 125

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 Ala Ala Ala Val Gln Lys Arg Val Glu Thr Val Ser Gln Thr Leu Arg
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 Ala Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala
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 Thr Thr Arg Ile Gly Asp Leu Ala Pro Gln Asp Met Lys Lys Val Cys
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 325 330 335

Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg

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345

350

Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly

355

360

365

Ala Ala Ile Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe

370

375

380

Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His Asp Ala Ala

385

390

395

400

Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser

405

410

415

Val Glu Tyr Leu Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys

420

425

430

Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp

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445

Ala Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val

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455

460

Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met

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475

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Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys Ser

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490

495

Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met

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510

His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe

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Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His Lys Lys Asp

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540

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 Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp
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 Asn Ser Thr Leu Ser Asp Ser Gly Met Ile Asp Asn Leu Pro Asp Ser
 20 25 30
 cca gac gag gta gcc aag gag ctg gag ctg ctc ggg gga tgg aca gat 143
 Pro Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp
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 Asp Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn
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 ggg gtc cag acc aat cca ttt ctg aat ggg aac gtg ccc gtc atg ccc 239
 Gly Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro
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 agc ctg gat gag ctg aat ccc aaa agt act gtg gat ttg ctc ctt ttt 287
 Ser Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe
 80 85 90 95
 gac gca ggt aca tcc tcc ttc acc gaa tcc agc tca gcc acc acg aat 335
 Asp Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn
 100 105 110
 agc act ggc aac atc ttc gat gag ctt cca gtc aca aac ggg ctc cac 383
 Ser Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His
 115 120 125
 gca gag ccg ccg gtc agg cgg gac aac ccc ttc ttc aga agc aag cgc 431
 Ala Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg
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 Ser Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala

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Pro Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu			
160	165	170	175
caa ttt cag agc cgg gag gat ttt cga act gcc tgg cta aac cac agg	575		
Gln Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg			
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Lys Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro			
195	200	205	
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Gly Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu			
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225	230	235	
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Met Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser			
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Cys Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val			
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Lys Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn			

290	295	300	
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Asp Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp			
305	310	315	
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Asp Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val			
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Ala Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp			
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Ala Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn			
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Pro Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu			
420	425	430	
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gaacaaacat tagctatitt atgctgcaag aaccaggaca cacaattcgc caatcatccc 4211
 accatataac cttegatitgt gcttctcaac tccaccccat aatttctccc agagatcatc 4271
 tatcaccttt tccccaaaga agaaacaaaa ccagttgcac cttaaaccat ggatattttt 4331
 tcttcagggg ctttaaataag ttctctatgc aacgtgtctt gtagcacaaa taaaattcta 4391
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 gtaccaacc agactttaaa taaaacaaac atgaaacct 4490

<210> 152

<211> 863

<212> PRT

<213> Homo sapiens

<400> 152

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Ser Thr Leu Ser Asp Ser Gly Met Ile Asp Asn Leu Pro Asp Ser Pro

20 25 30

Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp Asp

35 40 45

Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn Gly

50 55 60

Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro Ser

65 70 75 80

Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe Asp

85 90 95

Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn Ser

100 105 110

Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His Ala

115	120	125	
Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg Ser			
130	135	140	
Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala Pro			
145	150	155	160
Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu Gln			
165	170	175	
Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg Lys			
180	185	190	
Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro Gly			
195	200	205	
Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu Asp			
210	215	220	
Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile His			
225	230	235	240
Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser Met			
245	250	255	
Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser Cys			
260	265	270	
Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val Lys			
275	280	285	
Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp			
290	295	300	
Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp Ser			
305	310	315	320
Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly Asp			
325	330	335	

Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val Ala
 340 345 350
 Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp Asp
 355 360 365
 Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His Ile
 370 375 380
 His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys Ala
 385 390 395 400
 Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn Pro
 405 410 415
 Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu Ser
 420 425 430
 Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn Tyr
 435 440 445
 Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln Leu
 450 455 460
 Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln Asn
 465 470 475 480
 Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp Asp
 485 490 495
 Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro Pro
 500 505 510
 Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys
 515 520 525
 Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys
 530 535 540

Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys

545 550 555 560

Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu Glu

565 570 575

Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val Arg

580 585 590

Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr Gln

595 600 605

Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly Arg

610 615 620

Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val Leu

625 630 635 640

Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr Ala

645 650 655

Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser Phe

660 665 670

Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys Arg

675 680 685

Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu Lys

690 695 700

Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser Phe

705 710 715 720

Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly Leu

725 730 735

Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val Glu

740 745 750

Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val Ser

755	760	765	
Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn Gly			
770	775	780	
Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu Leu			
785	790	795	800
Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln Glu			
805	810	815	
Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg Trp			
820	825	830	
Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val Leu			
835	840	845	
Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile			
850	855	860	

<210> 153

<211> 2194

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133).. (1125)

<400> 153

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tgccttctcg ttctactgcc ccaggagccc ggcgggtccg ggactcccggt ccgtgccggt 120

gcgggcgcgcgc gc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc cct 171

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro

1

5

10

ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg gtc	219
Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val	
15 20 25	
aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc ttc	267
Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe	
30 35 40 45	
agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag ccc	315
Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro	
50 55 60	
cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac gcg	363
Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala	
65 70 75	
ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga gca	411
Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala	
80 85 90	
aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct gtc	459
Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val	
95 100 105	
tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg cga	507
Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg	
110 115 120 125	
ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca gca	555
Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala	
130 135 140	
aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc cta	603
Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu	

145	150	155	
agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc ttt			651
Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe			
160	165	170	
gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa atg			699
Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met			
175	180	185	
tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct ttc			747
Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe			
190	195	200	205
ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta ata			795
Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile			
210	215	220	
aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat ggg			843
Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly			
225	230	235	
aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg atg			891
Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met			
240	245	250	
gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg tgt			939
Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys			
255	260	265	
gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc tac			987
Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr			
270	275	280	285
ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act gtt			1035
Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val			

290	295	300	
aat acc ttt gat gaa aag agt tac tac gaa tcc cal ctt ggt tcc agc			1083
Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser			
305	310	315	
tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc			1125
Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe			
320	325	330	
tagacittca cgggtgggacg aaacgggttc agaaactgcc aggggcctca tacagggata			1185
tcaaaatacc ctttgtgcta gccagggccc tggggaatca ggtgactcac acaaagcaa			1245
tagttgggtca ctgcattttt acctgaacca aagctaaacc cgggtgttgcc accatgcacc			1305
atggcatgcc agagtccaac actgttgcctc ttgaaaatct gggctctgaaa aaacgcacaa			1365
gagccctgc cctgccctag ctgaggcaca caggagacc cagtgaggat aagcacagat			1425
tgaattgtac agtttgcaga tgcagatgta aatgcatggg acatgcatga taactcagag			1485
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gatttatagc atcttgaata gagagctgca aaccaccagg gggcagagtt gcatttttcc			1785
aggcttttta ggaagctctg caacagatgt gatcigtatca taggcaatta gaactggaag			1845
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gcaagacccc atctctaaaa aattagggcat ggtgggtgcat gccgtatttc ccagctactc			2085
aggaggttga ggtgggagga tcacttgagc ccagaagttc aaggctgcaa tgagccatga			2145
ttacaccacg gcactacaac ctgggtggca cagtigagaac ctgactctt			2194

<211> 331

<212> PRT

<213> Homo sapiens

<400> 154

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe

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Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys

20 25 30

Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu

35 40 45

Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg

50 55 60

Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn

65 70 75 80

Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val

85 90 95

Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His

100 105 110

Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp

115 120 125

Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg

130 135 140

Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala

145 150 155 160

Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys

165 170 175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu

180

185

190

Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu

195

200

205

Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

210

215

220

Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg

225

230

235

240

Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu

245

250

255

Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser

260

265

270

Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys

275

280

285

Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe

290

295

300

Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr

305

310

315

320

Asp Ser Met Val Glu Asp Cys Glu Pro His Phe

325

330

<210> 155

<211> 3377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44).. (1666)

<400> 155

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Met Leu Ser Pro

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cag cga gtg gga gca gct gcc tca aga gga gca gat gat gcc atg gag 103

Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp Asp Ala Met Glu

5 10 15 20

agc agc aag cct ggt cca gtg cag gtt gtt ttg gtt cag aaa gat caa 151

Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val Gln Lys Asp Gln

25 30 35

cat tcc ttt gag cta gat gag aaa gcc ttg gcc agc atc ctc ttg cag 199

His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser Ile Leu Leu Gln

40 45 50

gac cac atc cga gat ctt gat gtg gtg gtg gtt tca gtg gct ggt gcc 247

Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser Val Ala Gly Ala

55 60 65

ttc cga aag ggc aag tcc ttc att ctg gat ttt atg cta cga tac tta 295

Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met Leu Arg Tyr Leu

70 75 80

tat tct cag aag gaa agt ggc cat tca aat tgg ttg ggt gac cca gaa 343

Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu Gly Asp Pro Glu

85 90 95 100

gaa ccg tta aca gga ttt tcc tgg aga ggg gga tct gat cca gaa acc 391

Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser Asp Pro Glu Thr

105 110 115

act ggg att caa atc tgg agt gaa gtt ttc act gtg gag aag cca ggt 439

Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val Glu Lys Pro Gly
 120 125 130
 ggg aag aag gtt gca gtt gtt ctg atg gat acc cag ggg gca ttt gac 487
 Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln Gly Ala Phe Asp
 135 140 145
 agc cag tca act gtg aaa gac tgt gct acc atc ttt gct cta agc act 535
 Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe Ala Leu Ser Thr
 150 155 160
 atg act agt tct gtt cag att tat aat tta tct cag aac att caa gaa 583
 Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln Asn Ile Gln Glu
 165 170 175 180
 gat gat ctt caa cag ctg cag ctc ttc aca gaa tac ggt cgt ctg gca 631
 Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr Gly Arg Leu Ala
 185 190 195
 atg gat gaa att ttc caa aag cct ttc cag aca ctg atg ttt ttg gtt 679
 Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu Met Phe Leu Val
 200 205 210
 aga gat tgg agt ttc cct tat gaa tat agc tat gga ctc caa gga gga 727
 Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly Leu Gln Gly Gly
 215 220 225
 atg gca ttt ttg gat aag cgt tta cag gtg aag gaa cat caa cat gaa 775
 Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu His Gln His Glu
 230 235 240
 gaa att cag aat gtt cga aat cac att cac tca tgt ttc tcc gat gtc 823
 Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys Phe Ser Asp Val
 245 250 255 260

acc tgc ttt ctc tta cca cat cca gga ctc cag gtg gcc aca agc cct 871
 Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val Ala Thr Ser Pro
 265 270 275

gac ttt gat ggg aaa tta aaa gat att gct ggt gaa ttc aaa gag cag 919
 Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu Phe Lys Glu Gln
 280 285 290

tta cag gca ctg ata ccg tat gta tta aac cca tct aag tta atg gaa 967
 Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser Lys Leu Met Glu
 295 300 305

aag gag atc aat ggc tca aag gtc acc tgt cgg gga cta ctg gag tat 1015
 Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly Leu Leu Glu Tyr
 310 315 320

ttt aag gca tat att aaa att tat caa gga gaa gat ctg cct cac ccc 1063
 Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp Leu Pro His Pro
 325 330 335 340

aag tcc atg ctt cag gcc act gct gaa gcc aac aac tta gca gct gca 1111
 Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Ala
 345 350 355

gcc tct gcc aag gac att tat tat aac aac atg gaa gag gtt tgt ggg 1159
 Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu Glu Val Cys Gly
 360 365 370

gga gag aaa cct tat ttg tct cca gac att cta gag gag aag cac lgt 1207
 Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu Glu Lys His Cys
 375 380 385

gaa ttc aaa caa ctt gct ctg gac cat ttt aag aag acc aag aag atg 1255
 Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys Thr Lys Lys Met
 390 395 400

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 405 410 415 420
 atc aag gaa tta tat gag aac ttc tgc aag cac aat ggt agc aag aac 1351
 Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn Gly Ser Lys Asn
 425 430 435
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 440 445 450
 gct ttg tac ata gcc tca ggc ctc act ggc ttc ata ggt ctt gag gtt 1447
 Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile Gly Leu Glu Val
 455 460 465
 gla gcc cag ttg ttc aac tgt atg gtt gga cta ctg tta ata gca ctc 1495
 Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu Leu Ile Ala Leu
 470 475 480
 ctc acc tgg ggc tac atc agg tat tct ggt caa tat cgt gag ctg ggc 1543
 Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr Arg Glu Leu Gly
 485 490 495 500
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 Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu Gln Ala Ser Ser
 505 510 515
 cat atc ggt aat tcc act cag gcc act gtg agg gat gca gtt gtt gga 1639
 His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp Ala Val Val Gly
 520 525 530
 aga cca tcc atg gat aaa aaa gct caa tagcatccta acgtgaagat 1686
 Arg Pro Ser Met Asp Lys Lys Ala Gln

535

540

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ccatgtgacc tctgataagt cacttgaact tgtgcctag tcaggttcac tglaggltta 2826
catatgtatg tatgttttac acaactctg taattgtcat ttgaggggtt cacttctcc 2886
tcccacccc tggagcggc cctgcgtgt cactgacatc tattaataa aaaaaaaaaa 2946
ttgtctctca aggtgtttga ggcttlaatg caaccttta gcccttgggt ctttttggtg 3006
caagaattct ggtgttttac ctgacatca gaccttgaa atgttgcaa attcttcaaa 3066
taactgtttg ggggttggg ggagatgaaa gagatcgcg ttgtgttac agttaaagac 3126
atccaatac ttaaaaagga gtttctctt agaaacacac acaccttcc tctgtctaa 3186
aagatctac tccatgatac tgtgtaaaat attttgcac tgtgtgaag tatttttgac 3246

ttttttctgt acataactgt gtctcagag cigaatgitt atatcttttg ctgtgcaaaa 3306
 gaaacaigla aaatgttgtt cagttgtata tacagaaatg tgtataaaac attttgttat 3366
 tttttaaaag t 3377

<210> 156

<211> 541

<212> PRT

<213> Homo sapiens

<400> 156

Met Leu Ser Pro Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp

1 5 10 15

Asp Ala Met Glu Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val

20 25 30

Gln Lys Asp Gln His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser

35 40 45

Ile Leu Leu Gln Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser

50 55 60

Val Ala Gly Ala Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met

65 70 75 80

Leu Arg Tyr Leu Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu

85 90 95

Gly Asp Pro Glu Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser

100 105 110

Asp Pro Glu Thr Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val

115 120 125

Glu Lys Pro Gly Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln

130 135 140

Gly Ala Phe Asp Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe
 145 150 155 160
 Ala Leu Ser Thr Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln
 165 170 175
 Asn Ile Gln Glu Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr
 180 185 190
 Gly Arg Leu Ala Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu
 195 200 205
 Met Phe Leu Val Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly
 210 215 220
 Leu Gln Gly Gly Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu
 225 230 235 240
 His Gln His Glu Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys
 245 250 255
 Phe Ser Asp Val Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val
 260 265 270
 Ala Thr Ser Pro Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu
 275 280 285
 Phe Lys Glu Gln Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser
 290 295 300
 Lys Leu Met Glu Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly
 305 310 315 320
 Leu Leu Glu Tyr Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp
 325 330 335
 Leu Pro His Pro Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn
 340 345 350

Leu Ala Ala Ala Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu
355 360 365
Glu Val Cys Gly Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu
370 375 380
Glu Lys His Cys Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys
385 390 395 400
Thr Lys Lys Met Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu
405 410 415
Leu Glu Glu Glu Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn
420 425 430
Gly Ser Lys Asn Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe
435 440 445
Thr Gly Ile Val Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile
450 455 460
Gly Leu Glu Val Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu
465 470 475 480
Leu Ile Ala Leu Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr
485 490 495
Arg Glu Leu Gly Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu
500 505 510
Gln Ala Ser Ser His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp
515 520 525
Ala Val Val Gly Arg Pro Ser Met Asp Lys Lys Ala Gln
530 535 540

<210> 157

<211> 2172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45).. (563)

<400> 157

ggaacacggc acccgcacig cgcgtcatgg tgcaggcctg gtaa atg gac gac gcc 56

Met Asp Asp Ala

1

ccg ggc gac ccg cgg caa ccc cac cgc ccc gac ccc ggc cgc cca gtg 104

Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro Gly Arg Pro Val

5 10 15 20

ggc ctg gag cag ctg cgg cgg ctc ggg gtg ctc tac tgg aag ctg gat 152

Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp

25 30 35

gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga aga gag 200

Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu

40 45 50

agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat aaa cta 248

Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu

55 60 65

cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat ttg cac 296

Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His Leu His

70 75 80

ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac ttc gat 344

Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp

85 90 95 100

gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag aag gga 392
 Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu Lys Gly
 105 110 115
 gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg gtg gac 440
 Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp
 120 125 130
 gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa ccg gtg 488
 Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val
 135 140 145
 tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc ggg cag 536
 Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln
 150 155 160
 tac gtg aaa ttt ctg gca cag acc gcc tagcagtgt gccctgggaac 583
 Tyr Val Lys Phe Leu Ala Gln Thr Ala
 165 170
 taacacgtgc ctgttaaagg tccccaatgt aatgactgag cagaaaaatca atcacitct 643
 ctttgcitit agaggatagc ctgaggcta gattatcttt ccttltgaag attatttgat 703
 cagaatattt tgaatgaaa ggaactagaa agcaacttgg aagtglaaag agtcaccttc 763
 atttctgta actcaatcaa gactgggtggg tccatggccc tgggttagtt catgcatca 823
 gttgagtcce aatgaaagt ttcattctcc gaaatgcagt tccitagtatg cccatctgga 883
 cgtgatgccg cgccigccgt gtaagaaggt gcaatcctag ataacacagc tagccagata 943
 gaagacactt tttctccaa aatgatgcct tgggggtggg agtggtaggg ggaagagctc 1003
 ccaccctaag gggcacacac tgagttgctt atgccacttc ctgttcaaa ataaagtaac 1063
 tgccttaac ttatactcat ggcttggagt taccitatat tcaggatat gtgatatttt 1123
 gcctgglttg ttaaaatgc cccatttaga ttccttctat aattgttctt atagataagt 1183
 aatttatata tgagctgtgt tagtatitit tcaagtgtgag atctctggat tcttcacaa 1243

taaagctgtt gaattttaac aggagtatta gtacataaat tttctactca acaattccga 1303
 gataggattt tgcctagttt gtcatatcac agaaaaactc caagttaact tcatgttttg 1363
 gaagggcagg tcgtttttta agtattttctt tttttaactg gatgaaaaat cttcatgtta 1423
 ggattaattt tcttaatcac ctcacacacig tacagaggaa actcaagcct taaatgttta 1483
 agtaaacctt gtcctagttt taggattaaa ataccacaccg ggggtgtgat gatgccalat 1543
 accgcagggc ttgcttctgt caagtgtgac tctatctcag taattaaaat aagtgtgat 1603
 ctactgattt tttttaatgg attcatttct aaatgggcat tataaataga gcttggtcat 1663
 ttttaagaac gaaacattca tatgataaac tategcttta aattgccttt ctgcttcat 1723
 ataacttttc cctgtcagga tecttagtgt ttgaaactcc tcgtgcgggg ctggcctcct 1783
 gcggactcta gtttcgctc ctgtatgttg cgcctgggat ttcttactt cagagctgta 1843
 tttttacagg caagagtaag ttcttgggca cagtggctca tgcctgtaat ctgactact 1903
 caggaggcta aggtgggagg attcttagag cctgggaggt cgaggctgca gtgagctgtg 1963
 attgtggcca ctgcactcca gccctgggtga cagagcgaga ctctgtctca aaaaagaaga 2023
 aagagtaaga gctgaggcat ataatagaat tctgctaaag cacttaaggt gaaatcacat 2083
 tttcttttcc caggatgttg ctacatctt tcgtttttat tgaggigtca tttatgtaca 2143
 ataaaatgta ctcatittca gtgtttttg 2172

<210> 158

<211> 173

<212> PRT

<213> Homo sapiens

<400> 158

Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro

1

5

10

15

Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr

20

25

30

Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys

35	40	45
Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys		
50	55	60
Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu		
65	70	75
Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser		
85	90	95
Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe		
100	105	110
Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg		
115	120	125
Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val		
130	135	140
Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu		
145	150	155
Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala		
165	170	

<210> 159

<211> 20

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 159

ggaagtgta ctctgctct

20

<210> 160

<211> 50

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 160

gagagagaga gagagagaga actagtcctcg agtttttttt tttttttttt 50

<210> 161

<211> 41

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 161

gagagagaga gagagagcgg ccgcactagt cccccccccc c 41

<210> 162

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo-cap linker sequence

<400> 162

agcaucgagu cggccuuguu ggccuacugg 30

<210> 163

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo (dT) primer sequence

<400> 163

gcggctgaag acggcctatg tggccttttt tttttttttt tt 42

<210> 164
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer sequence
 <400> 164
 agcatcgagt cggccttggt g 21

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer sequence
 <400> 165
 gcggctgaag acggcctatg t 21

<210> 166
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer sequence
 <400> 166
 actttatgt catagtttag atctatttg 30

<210> 167
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer sequence
 <400> 167
 ataatcctta aaaactccat ttccaccct 30

<210> 168
 <211> 1536
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (139).. (1062)
 <400> 168
 GTGCTCCGCC GCCCGCCCCG ACCCGGGCCC AGCCGCCTCC ACGGCCCGCG CTCGTACTGG 60
 AGCGAAGAGC GGCCTCCTGA GGGAGGGGAA GGGACGTGGG GCGGCCACG GCAGGATTAA 120
 CCTCCATTTC AGCTAATC ATG GGA GAG ATT AAA GTC TCT CCT GAT TAT AAC 171
 Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn
 1 5 10

TGG TTT AGA GGT ACA GTT CCC CTT AAA AAG ATT ATT GTG GAT GAT GAT Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp 15 20 25	219
GAC AGT AAG ATA TGG TCG CTC TAT GAC GCG GGC CCC CGA AGT ATC AGG Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg 30 35 40	267
TGT CCT CTC ATA TTC CTG CCC CCT GTC AGT GGA ACT GCA GAT GTC TTT Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe 45 50 55	315
TTC CGG CAG ATT TTG GCT CTG ACT GGA TGG GGT TAC CGG GTT ATC GCT Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala 60 65 70 75	363
TTG CAG TAT CCA GTT TAT TGG GAC CAT CTC GAG TTC TGT GAT GGA TTC Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe 80 85 90	411
AGA AAA CTT TTA GAC CAT TTA CAA TTG GAT AAA GTT CAT CTT TTT GGC Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His Leu Phe Gly 95 100 105	459
GCT TCT TTG GGA GGC TTT TTG GCC CAG AAA TTT GCT GAA TAT ACT CAC Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His 110 115 120	507
AAA TCT CCT AGA GTC CAT TCC CTA ATC CTC TGC AAT TCC TTC AGT GAC Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp 125 130 135	555
ACC TCT ATC TTC AAC CAA ACT TGG ACT GCA AAC AGC TTT TGG CTG ATG Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met 140 145 150 155	603
CCT GCA TTT ATG CTC AAA AAA ATA GTT CTT GGA AAT TTT TCA TCT GGC Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly 160 165 170	651
CCG GTG GAC CCT ATG ATG GCT GAT GCC ATT GAT TTC ATG GTA GAC AGG Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg 175 180 185	699
CTA GAA AGT TTG GGT CAG AGT GAA CTG GCT TCA AGA CTT ACC TTG AAT Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn 190 195 200	747
TGT CAA AAT TCT TAT GTG GTA CCT CAT AAA ATT CGG GAC ATA CCT GTA Cys Gln Asn Ser Tyr Val Val Pro His Lys Ile Arg Asp Ile Pro Val 205 210 215	795

ACT ATT ATG GAT GTG TTT GAT CAG AGT GCG CTT TCA ACT GAA GCT AAA 843
 Thr Ile Met Asp Val Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys
 220 225 230 235

 GAA GAA ATG TAC AAG CTG TAT CCT AAT GCC CGA AGA GCT CAT CTG AAA 891
 Glu Glu Met Tyr Lys Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys
 240 245 250

 ACA GGA GGC AAT TTC CCA TAC CTG TGC AGA AGT GCA GAG GTC AAT CTT 939
 Thr Gly Gly Asn Phe Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu
 255 260 265

 TAT GTA CAG ATA CAT TTG CTG CAA TTC CAT GGA ACC AAA TAC GCG GCC 987
 Tyr Val Gln Ile His Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala
 270 275 280

 ATT GAC CCA TCA ATG GTC AGT GCC GAG GAG CTT GAG GTG CAG AAA GGC 1035
 Ile Asp Pro Ser Met Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly
 285 290 295

 AGC CTT GGC ATC AGC CAG GAG GAG CAG TAGTGTGTCT CTCGCTGTCA ATGATGA 1089
 Ser Leu Gly Ile Ser Gln Glu Glu Gln
 300 305

 GTTGACCCGG TGTGTTCTTG TATAGTCAGT GGCATCAGCA CCCGTCAGCC GGCCTTTTCC 1149
 TTCAGGTTTCG TCAGGCTCAC CGGTTCTCAC TGTGTCTGGG AAGTAGGACT GATGCTCATC 1209
 TTCATGACAG GCGGCATCTC CACTAAGCCT GTGTAAGTGT TCCCTCTTTG GTTTTCTTAG 1269
 CTTTTGAATT TGAAGAAGTA CTTTGAAGA CTCCCATTTT AAGAACCGTG CAGATTTTGC 1329
 TACCAAAAGT CTTCAACCACT GTGTTCTTAA GTGAATGTTA ATTTCTGAGG TTTGGGACTT 1389
 TGTGGTGGTT TTTTCTTCT TTTCTTTTCC ATTCTTCTTT CTTTCTTTT ATGTTGTTTG 1449
 CTGTAAATGC TGCACATCCA GATTGCATAT CAGGACATTG GTTATTTTAT GCTTCTTGG 1509
 ATATAACCAT GATCAGAGTG CCATGGC 1536

<210> 169

<211> 308

<212> PRT

<213> Homo sapiens

<400> 169

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr
 1 5 10 15
 Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Asp Ser Lys Ile Trp
 20 25 30
 Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe
 35 40 45
 Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu
 50 55 60
 Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val
 65 70 75 80
 Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp
 85 90 95
 His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly
 100 105 110
 Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val

115 120 125
 His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn
 130 135 140
 Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu
 145 150 155 160
 Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met
 165 170 175
 Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly
 180 185 190
 Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn Cys Gln Asn Ser Tyr
 195 200 205
 Val Val Pro His Lys Ile Arg Asp Ile Pro Val Thr Ile Met Asp Val
 210 215 220
 Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys Glu Glu Met Tyr Lys
 225 230 235 240
 Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys Thr Gly Gly Asn Phe
 245 250 255
 Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu Tyr Val Gln Ile His
 260 265 270
 Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala Ile Asp Pro Ser Met
 275 280 285
 Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly Ser Leu Gly Ile Ser
 290 295 300
 Gln Glu Glu Gln
 305

<210> 170

<211> 2560

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

(202).. (1002)

<400> 170

CTGGCCTACT GGGGCTCCAG CCGTGTCTTG AGGAGCTGGA CCAGCCACAT CCCCTGGGGC 60
 TGCAGTTGAA GCAGAACCAA GTGGCCATCC CGGCGTTAGA CCGTAGGTTC CTGGTCCCGG 120
 AGTGGTCGGA GCGCGCCAGT GGGCAGGCAG CTCTTGCTCA CAGGCCGCGG TGCCCAAGGC 180
 GCTGGCTCTC CGCAGGGCGG A ATG GCG CTG CAA GTG GAG CTG GTA CCC ACC 231

Met Ala Leu Gln Val Glu Leu Val Pro Thr
 1 5 10

GGG GAG ATC ATC CGC GTG GTT CAT CCC CAC AGG CCC TGC AAG CTT GCC 279
 Gly Glu Ile Ile Arg Val Val His Pro His Arg Pro Cys Lys Leu Ala
 15 20 25

CTG GGC AGT GAC GGG GTT CGG GTG ACC ATG GAG AGT GCG CTC ACC GCC 327
 Leu Gly Ser Asp Gly Val Arg Val Thr Met Glu Ser Ala Leu Thr Ala
 30 35 40

CGT GAC CGG GTG GGG GTG CAG GAT TTC GTG CTG CTG GAG AAC TTC ACC 375
 Arg Asp Arg Val Gly Val Gln Asp Phe Val Leu Leu Glu Asn Phe Thr
 45 50 55

AGC GAG GCC GCC TTC ATC GGG AAC CTG CGG CGG CGA TTT CGG GAG AAT Ser Glu Ala Ala Phe Ile Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn 60 65 70	423
CTC ATC TAC ACC TAC ATT GGC CCC GTC CTG GTC TCT GTC AAT CCC TAC Leu Ile Tyr Thr Tyr Ile Gly Pro Val Leu Val Ser Val Asn Pro Tyr 75 80 85 90	471
CGG GAC CTG CAG ATC TAC AGC CGG CAG CAT ATG GAG CGT TAC CGT GGC Arg Asp Leu Gln Ile Tyr Ser Arg Gln His Met Glu Arg Tyr Arg Gly 95 100 105	519
GTC AGC TTC TAT GAA GTG CCC CCT CAC CTG TTT GCC GTG GCG GAC ACT Val Ser Phe Tyr Glu Val Pro Pro His Leu Phe Ala Val Ala Asp Thr 110 115 120	567
GTG TAC CGA GCA CTG CGC ACG GAG CGT CGG GAC CAG GCT GTG ATG ATC Val Tyr Arg Ala Leu Arg Thr Glu Arg Arg Asp Gln Ala Val Met Ile 125 130 135	615
TCT GGG GAG AGC GGG GCA GGC AAG ACC GAG GCC ACC AAG AGG CTG CTG Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu 140 145 150	663
CAG TTC TAT GCA GAG ACC TGC CCA GCC CCC GAG CGC GGA GGT GCC GTG Gln Phe Tyr Ala Glu Thr Cys Pro Ala Pro Glu Arg Gly Gly Ala Val 155 160 165 170	711
CGG GAC CGG CTG CTA CAG AGC AAC CCG GTG CTG GAG GCC TTT GGA AAT Arg Asp Arg Leu Leu Gln Ser Asn Pro Val Leu Glu Ala Phe Gly Asn 175 180 185	759
GCC AAG ACC CTC CGG AAC GAT AAC TCC AGC AGG TTC GGG AAG TAC ATG Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met 190 195 200	807
GAT GTG CAG TTT GAC TTC AAG GGT GCC CCC GTG GGT GGC CAC ATC CTC Asp Val Gln Phe Asp Phe Lys Gly Ala Pro Val Gly Gly His Ile Leu 205 210 215	855
AGT TAC CCC CTG GAA AAG TCA CGA GTG GTG CAC CAG AAT CAT GGG GAG Ser Tyr Pro Leu Glu Lys Ser Arg Val Val His Gln Asn His Gly Glu 220 225 230	903
CGG AAC TTC ACA TCT TCT ACC AGC TGC TGG AGG GGG GCG AGG AGG AGA Arg Asn Phe Thr Ser Ser Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg 235 240 245 250	951
CTC TTC GCA GGC TGG GCT TGG AAC GGA ACC CCC AGA GCT ATC TGT ACC Leu Phe Ala Gly Trp Ala Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr 255 260 265	999
TGG TGAAGGCCAG TGTGCCAAAG TCTTCTTCAT CAACGACAAG AGTGACTGGA AGGTCG	1058

Trp

TCAGGAAGGC	TCTGACAGTC	ATTGATTTC	CCGAGGATGA	AGTGGAGGAC	CTGCTGAGCA	1118
TCGTGGCCAG	CGTCCTTCAT	TTGGGCAACA	TCCACTTTGC	TGCCAACGAG	GAGAGCAATG	1178
CCCAGGTCAC	CACCGAGAAC	CAGCTCAAGT	ATCTGAGCCC	ATTCAGTATG	CGGTGCCTGT	1238
TGTGAAATAC	GACCGCAAGG	GCTACAAGCC	TCGCTCCCGG	CAGCTGCTGC	TCACGCCCAA	1298
CGCCGTCGTC	ATCGTGGAGG	ACGCCAAAGT	CAAGCAGAGG	ATTGATTACG	CCAACCTGAC	1358
CGGAATCTCT	GTCAGCAGCC	TGAGCGACAG	TCTTTTTGTG	CTTCATGTAC	AGCGTGCGGA	1418
CAATAAGCAA	AAGGGAGATG	TGGTGCTGCA	GAGTGACCAC	GTGATTGAGA	CGCTGACCAA	1478
GACAGCCCTC	AGTGCCAACC	GCGTGAACAG	CATCAACATC	AACCAGGGCA	GCATCACGTT	1538
TGCAGGGGGC	CCCGGCAGGG	ATGGCACCAT	TGACTTCACA	CCCGGCTCGG	AGCTGCTCAT	1598
CACCAAGGCC	AAGAACGGGC	ACCTGGCTGT	GGTCGCCCCA	CGGCTGAATT	CTCGGTGATA	1658
AAGGCGCCCA	CTGGACCCTC	CCAACGCCCA	ATGCTTTGCT	TTTCTCCTCC	TCCCCTTCCC	1718
AGTTACCAAA	GACTCGAACT	TCCAGACAGG	GACCCAGGGA	CACCCCGAAG	CCCACCTGCA	1778
ATCTCCCACC	TCCTGCCCAT	CCCTCTCTTG	AGGGAGCAGC	AGGGGCCAGG	AGCTACCCCA	1838
GGAGTGGGCC	AGGCCGGGCC	ACAGCAATAG	GAAAGCCAGG	GCCAGAGCGA	GCCATGCCAG	1898
CCCTACTGCC	GATGCCAAAT	ATTTGAGAGA	AGGGAACTTT	TGCTGAGGTT	TTCTCTGAGG	1958
TTTTTTTTGA	TGCTTTATAG	GAAACTATTT	TTTAAAAAAA	GCCATTTCCC	ACCCAAGGAC	2018
ACAGTGGATG	TGTTTTCCCT	GACTCCAGCA	GGGCAAGGAA	ATGTAGCCGA	GAGGTTGTGT	2078
GGGCTGGGCT	CTGGTGCCTT	CTTCCCTGGC	CAGGACACCT	CTCCTCCTGA	TTCCCTTGGC	2138
ACCTTGTCTT	TCTGTCTGTT	TACCTGTCTC	CCTGCCTGCC	CATCTGCATC	TTTTGCAGCC	2198
CACTCTGACT	TCCATCTGGG	GGCTGAGACC	ACCTTGCCT	GCCCCCTTCT	TTCTGCCTTA	2258
AGAATGTCTT	TTTAGGCTGG	GCATGGTGCC	TCACGCCTGT	AACCCAGCA	CTTTGGGAGG	2318
CGGAGACGGG	CAGATAACCT	GAGGTCAGGA	TTTCGAGACC	AACCTGACCT	ACATGGAGAA	2378
ACTCCGCCTC	TGGTAAGGAT	ACAAAATTAG	CCGGGCATGG	TGGTGCACGC	CTCTAATCCC	2438
AGCTGCTCGG	GAGGCTGAGG	CAGGAGAATC	ACTTGAACCC	GGGAAGTGGA	GGTTGCAGTG	2498
AGCCAAGAGT	ACACCACTGC	ACTCCAGCCT	GGGCAACAGA	GCGAGACTCC	GTCTTAAAAA	2558
AA						2560

<210> 171

<211> 267

<212> PRT

<213> Homo sapiens

<400> 171

Met Ala Leu Gln Val Glu Leu Val Pro Thr Gly Glu Ile Ile Arg Val
1 5 10 15
Val His Pro His Arg Pro Cys Lys Leu Ala Leu Gly Ser Asp Gly Val
20 25 30
Arg Val Thr Met Glu Ser Ala Leu Thr Ala Arg Asp Arg Val Gly Val
35 40 45
Gln Asp Phe Val Leu Leu Glu Asn Phe Thr Ser Glu Ala Ala Phe Ile
50 55 60
Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn Leu Ile Tyr Thr Tyr Ile
65 70 75 80
Gly Pro Val Leu Val Ser Val Asn Pro Tyr Arg Asp Leu Gln Ile Tyr
85 90 95
Ser Arg Gln His Met Glu Arg Tyr Arg Gly Val Ser Phe Tyr Glu Val
100 105 110
Pro Pro His Leu Phe Ala Val Ala Asp Thr Val Tyr Arg Ala Leu Arg
115 120 125
Thr Glu Arg Arg Asp Gln Ala Val Met Ile Ser Gly Glu Ser Gly Ala
130 135 140
Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu Gln Phe Tyr Ala Glu Thr

GGG GCG GGG AAG GAA GAA GCG GAG GTC AAG GTG GAG CAG GAG AGG GAG Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu 100 105 110	454
ATA GAA AGC GAG GCA GGG GAA GAG AGT GAG TCG GAG GAA GAG AGC GAG Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu 115 120 125	502
TCA GAG GAA GAG AGC GAG ACA GAG GAA GAG AGT GAG GAT GAG AGC GAT Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp 130 135 140 145	550
GAG GAG AGT GAA GAA GAC AGC GAG GAA GAA ATG GAG GAT GAG CAA GAA Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu 150 155 160	598
AGC GAG GCC GAA GAA GAC AAC CAA GAA GAA GGG GAA TCC GAG GCG GAG Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu 165 170 175	646
GGA GAA ACT GAG GCA GAA AGT GAA TTT GAC CCA GAA ATA GAA ATG GAA Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu 180 185 190	694
GCA GAG AGA GTG GCC AAG AGG AAG TGT CCG GAC CAT GGG CTT GAT TTG Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu 195 200 205	742
AGT ACC TAT TGC CAG GAA GAT AGG CAG CTC ATC TGT GTC CTG TGT CCA Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro 210 215 220 225	790
GTC ATT GGG GCT CAC CAG GGC CAC CAA CTC TCC ACC CTA GAC GAA GCC Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala 230 235 240	838
TTT GAA GAA TTA AGA AGC AAA GAC TCA GGT GGA CTG AAG GCC GCT ATG Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met 245 250 255	886
ATC GAA TTG GTG GAA AGG TTG AAG TTC AAG AGC TCA GAC CCT AAA GTA Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val 260 265 270	934
ACT CGG GAC CAA ATG AAG ATG TTT ATA CAG CAG GAA TTT AAG AAA GTT Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val 275 280 285	982
CAG AAA GTG ATT GCT GAT GAG GAG CAG AAG GCC CTT CAT CTA GTG GAC Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp 290 295 300 305	1030
ATC CAA GAG GCA ATG GCC ACA GCT CAT GTG ACT GAG ATA CTG GCA GAC	1078

Ile Gln Glu Ala Met Ala Thr Ala His Val Thr Glu Ile Leu Ala Asp
 310 315 320

ATC CAA TCC CAC ATG GAT AGG TTG ATG ACT CAG ATG GCC CAA GCC AAG 1126
 Ile Gln Ser His Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys
 325 330 335

GAA CAA CTT GAT ACC TCT AAT GAA TCA GCT GAG CCA AAG GCA GAG GGC 1174
 Glu Gln Leu Asp Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly
 340 345 350

GAT GAG GAA GGA CCC AGT GGT GCC AGT GAA GAA GAG GAC ACA TGAAGGCTT 1225
 Asp Glu Glu Gly Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr
 355 360 365

GCTACCCCCA GTGGAAAATC ATCCCCTCCC CTTGTGTGTA TGTGACAGCG TGTATGTAAC 1285
 GGCTTCTGAT TTCTGTGAAA GCTGCTCAGC AACAAACGTA CTTCCACCAG ATGTGTCCCC 1345
 AGATCCACAG CAGGCACATA TCTCTCCAAG GGATGACCAG TTTTATGCTT ACTGTGTGCT 1405
 TCTCATCCCC TGGTTGTGGT AGGTCAAGGA AAAGAGCCCC TTTGATCCAC CAGGAGCAAT 1465
 TAAGAAAGGT CCTTCAGGTA ATCCCTCAAT GGCTGCTTTG AACTTACTCA GGAAAGCCAG 1525
 CCCCCATAAT ATTGTATTAC CAAACAGTAT CGCTTTGTTA GGAAGGATCT GGAATAATCT 1585
 TGAAGGGAAG TCAGAGTTTT CTCCCTGCCT ATTAACAAAA ACCCAATTTT GTTCATATTG 1645
 AAGCATGAAA TAAATGAGAG CAAGGTAGGG CCAAATTAAC TCTTGTGGAC AGTCCCTAAA 1705
 AGTCCAGTTC TACATTTGTG AAAATTGTGG TGCCATGAAT TAAGATGGAT GACTGGAAAA 1765
 AGGTGTTGGA GAAAGAGTTA AAGATGAGGA AGAGATATTT TTAGTATATG AAGTTATCCA 1825
 GGAATTGATA TTCATAATTC AGTGCTGTGG AAATGAAAAA AATGATTGAA GAGGTGGAAC 1885
 GGAAATGACC TTAGGGGGAA AAAAAAGGAC CAAAGAAGTC TGATTAAAAG TTGAAATCAG 1945
 TATTTCTGAA TTCAAATTGC TTGAATTTC AAAATAGTCA GTAAAGGATC TAATAGAACC 2005
 AGAATTATTT GGGTGAATTC TGCAGGTTTT ATGGGCTTGT CACAACGTGA AGGGCTGGAA 2065
 TGTATATTAC CAAATGGGAA TTTCCATTGT AGGTTTTTGC TAGTCCCACC CCCATTTTAG 2125
 CCTAATTTGG CTAAACGCA GTATGGGAG AATTGTTCCC ATTCCATGTG TTCTGAATTC 2185
 AGTCATCTC CCAGCATATA GATATATCCT CCTTTAACTC CGACCAGAAC CCTTCTTCCT 2245
 GTGGCACTCC CCACCCATAG ACCTTCAGAT CATCTCCAC ACCCTGGATC TCACTCTCCT 2305
 CTTAGTAACA GAGACACTCC TGAGGTGGA CTTCCTTGCT TTTCTCTACT TCCAAATCAC 2365
 AATTTCTTAC AACCAAGCTT TGTGCTCCCG AGTAAGCAGG GATGTACTAG GGGAATGTAA 2425
 AACTGCAAAC TTA AAAACCT GCATCTTCTT GAAGCATCAG TTTTACTTAC CAAATGTTT 2485
 AGAGTCATAA GATGACCTAT TTTTATATAA AAGTTATATT ATAGAATAAA ATGTTCATAC 2545
 GCATAGACTG TTAAG 2560

<210> 173

<211> 367

<212> PRT

<213> Homo sapiens

173

Met Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro
 1 5 10 15
 Trp Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe
 20 25 30
 Glu Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu
 35 40 45
 Ala Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys
 50 55 60
 Arg Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu

65		70		75		80									
Ala	Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly
				85					90					95	
Glu	Gly	Ala	Gly	Lys	Glu	Glu	Ala	Glu	Val	Lys	Val	Glu	Gln	Glu	Arg
			100					105					110		
Glu	Ile	Glu	Ser	Glu	Ala	Gly	Glu	Glu	Ser	Glu	Ser	Glu	Glu	Glu	Ser
		115					120					125			
Glu	Ser	Glu	Glu	Glu	Ser	Glu	Thr	Glu	Glu	Glu	Ser	Glu	Asp	Glu	Ser
	130					135					140				
Asp	Glu	Glu	Ser	Glu	Glu	Asp	Ser	Glu	Glu	Glu	Met	Glu	Asp	Glu	Gln
145					150					155				160	
Glu	Ser	Glu	Ala	Glu	Glu	Asp	Asn	Gln	Glu	Glu	Gly	Glu	Ser	Glu	Ala
			165					170					175		
Glu	Gly	Glu	Thr	Glu	Ala	Glu	Ser	Glu	Phe	Asp	Pro	Glu	Ile	Glu	Met
		180						185					190		
Glu	Ala	Glu	Arg	Val	Ala	Lys	Arg	Lys	Cys	Pro	Asp	His	Gly	Leu	Asp
	195						200					205			
Leu	Ser	Thr	Tyr	Cys	Gln	Glu	Asp	Arg	Gln	Leu	Ile	Cys	Val	Leu	Cys
	210					215					220				
Pro	Val	Ile	Gly	Ala	His	Gln	Gly	His	Gln	Leu	Ser	Thr	Leu	Asp	Glu
225					230					235				240	
Ala	Phe	Glu	Glu	Leu	Arg	Ser	Lys	Asp	Ser	Gly	Gly	Leu	Lys	Ala	Ala
			245						250				255		
Met	Ile	Glu	Leu	Val	Glu	Arg	Leu	Lys	Phe	Lys	Ser	Ser	Asp	Pro	Lys
		260						265					270		
Val	Thr	Arg	Asp	Gln	Met	Lys	Met	Phe	Ile	Gln	Gln	Glu	Phe	Lys	Lys
	275						280					285			
Val	Gln	Lys	Val	Ile	Ala	Asp	Glu	Glu	Gln	Lys	Ala	Leu	His	Leu	Val
	290					295					300				
Asp	Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala
305					310					315				320	
Asp	Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala
				325						330				335	
Lys	Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu
			340						345				350		
Gly	Asp	Glu	Glu	Gly	Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr	
	355						360					365			

<210> 174

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: a synthetic DNA

<400> 174

ttaagcttgc caccatgagc aaccccagcg ccccaccacc a

41

<210> 175

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 175

gtatcgattt aattgcgac ccccatcag

29

176

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 176

cacctactgtatgacaccacattc

24

<210> 177

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 177

gagatgcctgttccatgcctggcctg

24

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 178

ggaaaagctctccgtggctaacaag

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 179

catagtccttgacaagggtcacag

24

<210> 180

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 180

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22

<210> 181

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 181

ttcaccaccttcttgatgtcatcata

26

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06840

A. CLASSIFICATION OF SUBJECT MATTER

Int.Cl⁷ C12N15/12, C07K14/435, 16/18, C12P21/02,
C12Q1/68, A61K38/00, 39/395, 48/00, A61P9/10,
G01N33/50, 33/53,

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int.Cl⁷ C12N15/11-15/62, C07K14/00-14/825

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq,
BIOSIS (DIALOG), WPI (DIALOG)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO, 99/14327, A2 (GENENTECH, INC.), 25 March, 1999 (25.03.99), especially, PRO246, FIG.26 (Accession No.X28436), FIG.27 (Accession No.Y05286) & AU, 9893121, A & ZA, 9808293, A	2, 4, 11, 12, 36-40, 43, 45, 46
X	WO, 99/14328, A2 (GENENTECH, INC.), 25 March, 1999 (25.03.99), especially, FIGURE 16 (Accession No.X52221), FIGURE 17 (Accession No.Y13351) & ZA, 9808460, A & AU, 9893178, A & EP, 1027434, A2	2, 4, 11, 12, 36-40, 43, 45, 46
X	US, 5942606, A (INCYTE PHARMACEUTICALS, INC.), 24 August, 1999 (24.08.99), especially, SEQ ID NO:2 (Accession No.X87000), SEQ ID NO:1 (Accession No.Y27096) (Family: none)	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 99/58660, A1 (HUMAN GENOME SCIENCES, INC.), 18 November, 1999 (18.11.99),	2, 4, 11, 12, 36-40, 43,

☒ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:
 "A" document defining the general state of the art which is not
 considered to be of particular relevance
 "E" earlier document but published on or after the international filing
 date
 "L" document which may throw doubts on priority claim(s) or which is
 cited to establish the publication date of another citation or other
 special reason (as specified)
 "O" document referring to an oral disclosure, use, exhibition or other
 means
 "P" document published prior to the international filing date but later
 than the priority date claimed

"T" later document published after the international filing date or
 priority date and not in conflict with the application but cited to
 understand the principle or theory underlying the invention
 "X" document of particular relevance; the claimed invention cannot be
 considered novel or cannot be considered to involve an inventive
 step when the document is taken alone
 "Y" document of particular relevance; the claimed invention cannot be
 considered to involve an inventive step when the document is
 combined with one or more other such documents, such
 combination being obvious to a person skilled in the art
 "&" document member of the same patent family

Date of the actual completion of the international search
19 December, 2000 (19.12.00)

Date of mailing of the international search report
26 December, 2000 (26.12.00)

Name and mailing address of the ISA/
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06840

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	especially, SEQ ID NO:39 (Accession No.Z65278), SEQ ID NO:291 (Accession No.Y76303) & AU, 9938831, A	45,46
P,X	WO, 00/11015, A1 (ALPHAGENE, INC.), 02 March, 2000 (02.03.00), especially, SEQ ID NO:37 (Accession No.A23441), SEQ ID NO:38 (Accession No.Y94999) & AU, 9957847, A	2,4,11,12, 36-40,43, 45,46
P,X	WO, 00/15666, A2 (GENENTECH, INC.), 23 March, 2000 (23.03.00), especially, FIGURE 15 (Accession No.A30052), FIGURE 16 (Accession No.Y88574) & AU, 9958167, A	2,4,11,12, 36-40,43, 45,46
A	TOPPER, James N. et al., "Blood flow and vascular gene expression: fluid shear stress as a modulator of endothelial phenotype", Molecular Medicine Today, January, 1999, Volume 5, Number 1, pages 40-46	1,2,4-12, 35-50
A	ANDO, Joji et al., "Flow-dependent Regulation of Gene Expression in Vascular Endothelial Cells", Japanese Heart Journal, January, 1996, Volume 37, Number 1, 19-32	1,2,4-12, 35-50

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06840

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 22,33,51,57,66,69,76

because they relate to subject matter not required to be searched by this Authority, namely:

The inventions as set forth in claims 22, 33, 66 and 69 relate to "methods for inhibiting, promoting or controlling cell apoptosis". As stated in the description, these methods are performed for therapy in the human body. Therefore, these inventions pertain to methods for treatment of the human body by therapy. The inventions as set forth in claims 51, 57 and 76 relate to "drug delivery methods for inducing a fused antibody comprising an antibody bonded to a drug into arteriosclerotic focus" which are to be performed in the human body in therapy. Therefore, these inventions pertain to methods for treatment of the human body by therapy.

2. ☐ Claims Nos.:

because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:

because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See extra sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

The inventions as set forth in claims which relate to the base sequence represented by SEQ ID NO:143 or the amino acid sequence represented by SEQ ID NO:144

- Remark on Protest** ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

第I欄1. の続き

薬剤とを結合させた融合抗体を動脈硬化巣へ誘導するドラッグデリバリー法」に関するものであり、ヒトを治療する際に体内で実施されるものであるから、人の身体の治療による処置方法に該当する。

第II欄の続き

, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109で表される塩基配列(若しくは、配列番号144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110で表されるアミノ酸配列)、又は、配列番号115, 116, 129, 130, 131, 132, 133, 134で表される塩基配列、のそれぞれに関連した発明に共通する事項は、「血管内皮細胞においてずり応力刺激により発現が誘導されるDNA」ということである。しかしながら、「血管内皮細胞においてずり応力刺激により発現が誘導されるDNA」としては、出願人も認識しているように endothelin-1 や monocyte chemotactic protein-1 などが既に公知であったから、請求の範囲に記載された上記各塩基配列(又は、アミノ酸配列)に関連した発明に共通する「特別な技術的特徴」は存在しないといえる。

したがって、請求の範囲には、配列番号143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109で表される塩基配列(若しくは、配列番号144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110で表されるアミノ酸配列)、又は、配列番号115, 116, 129, 130, 131, 132, 133, 134で表される塩基配列、のそれぞれに関連した別異の86発明が包含されている。

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06840

Continuation of Box No.II of continuation of first sheet(1)

The requirement of unity of invention in international application (PCT Rule 13.1) is not satisfied unless there is a technical relationship between a group of inventions as set forth in claims involving one or more of the same or corresponding special technical feature. The term "special technical feature" means a technical feature clearly showing the contribution achieved by the inventions as set forth in the claims as a whole (PCT Rule 13.2). The requirement of unity of invention is judged without considering whether the group of inventions are described in separate claims or in a single claim in the alternative form (PCT Rule 13.3).

In the present case, the inventions relating to the base sequences represented by SEQ ID NOS: 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 and 109 (or the amino acid sequences represented by SEQ ID NOS:144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108 and 110) or the base sequences represented by SEQ ID NO:115,116, 129, 130, 131, 132, 133 and 134 have a matter in common "DNA the expression of which is induced by a shear stress stimulus in hemoendothelial cells". However, there had been publicly known endothelin-1, monocyte chemotactic protein-1, etc. as "DNA the expression of which is induced by a shear stress stimulus in hemoendothelial cells", as the applicant recognizes. Therefore, it can be concluded that there is no "special technical feature" common to the inventions relating to the above-described base sequences (or amino acid sequences) as set forth in the claims.

Such being the case, the claims involve 86 separate inventions respectively relating to the base sequences represented by SEQ ID NOS: 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 and 109 (or the amino acid sequences represented by SEQ ID NOS:144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108 and 110) or the base sequences represented by SEQ ID NO:115,116, 129, 130, 131, 132, 133 and 134.

A. 発明の属する分野の分類 (国際特許分類 (IPC))

Int. Cl⁷ C12N15/12, C07K14/435, 16/18, C12P21/02,
C12Q1/68, A61K38/00, 39/395, 48/00, A61P9/10,
G01N33/50, 33/53,

B. 調査を行った分野

調査を行った最小限資料 (国際特許分類 (IPC))

Int. Cl⁷ C12N15/11-15/62, C07K14/00-14/825

最小限資料以外の資料で調査を行った分野に含まれるもの

国際調査で使用了電子データベース (データベースの名称、調査に使用した用語)

GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq,
BIOSIS (DIALOG), WPI (DIALOG)

C. 関連すると認められる文献

引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
X	WO, 99/14327, A2 (GENENTECH, INC.) 25.3月.1999 (25.03.99) 特に、PRO246, FIG.26(Accession No.X28436), FIG.27(Accession No.Y05286) & AU, 9893121, A & ZA, 9808293, A	2, 4, 11, 12, 36-40, 43, 45, 46
X	WO, 99/14328, A2 (GENENTECH, INC.) 25.3月.1999 (25.03.99) 特に、FIGURE 16(Accessiion No.X52221),	2, 4, 11, 12, 36-40, 43, 45, 46

☒ C欄の続きにも文献が列挙されている。☐ パテントファミリーに関する別紙を参照。

* 引用文献のカテゴリー

「A」特に関連のある文献ではなく、一般的技術水準を示すもの

「E」国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの

「L」優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献 (理由を付す)

「O」口頭による開示、使用、展示等に言及する文献

「P」国際出願日前で、かつ優先権の主張の基礎となる出願

の日の後に公表された文献

「T」国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの

「X」特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの

「Y」特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの

「&」同一パテントファミリー文献

国際調査を完了した日

19.12.00

国際調査報告の発送日

26.12.00

国際調査機関の名称及びあて先

日本国特許庁 (ISA/JP)

郵便番号100-8915

東京都千代田区霞が関三丁目4番3号

特許庁審査官 (権限のある職員)

内田 俊生

4N

8214

電話番号 03-3581-1101 内線 3488

C (続き) 関連すると認められる文献		
引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
	FIGURE 17 (Accession No. Y13351) & ZA, 9808460, A & AU, 9893178, A & EP, 1027434, A2	
X	US, 5942606, A (INCYTE PHARMACEUTICALS, INC.) 24.8月.1999 (24.08.99) 特に、SEQ ID NO:2 (Accession No. X87000), SEQ ID NO:1 (Accession No. Y27096) (ファミリーなし)	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 99/58660, A1 (HUMAN GENOME SCIENCES, INC.) 18.11月.1999 (18.11.99) 特に、SEQ ID NO:39 (Accession No. Z65278), SEQ ID NO:291 (Accession No. Y76303) & AU, 9938831, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/11015, A1 (ALPHAGENE, INC.) 2.3月.2000 (02.03.00) 特に、SEQ ID NO:37 (Accession No. A23441), SEQ ID NO:38 (Accession No. Y94999) & AU, 9957847, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/15666, A2 (GENENTECH, INC.) 23.3月.2000 (23.03.00) 特に、FIGURE 15 (Accession No. A30052), FIGURE 16 (Accession No. Y88574) & AU, 9958167, A	2, 4, 11, 12, 36-40, 43, 45, 46
A	TOPPER, James N. et al., "Blood flow and vascular gene ex- pression: fluid shear stress as a modulator of endothelial phenotype", Molecular Medicine Today, January, 1999, Volume 5, Number 1, pages 40-46	1, 2, 4-12, 35-50
A	ANDO, Joji et al., "Flow-dependent Regulation of Gene Ex- pression in Vascular Endothelial Cells", Japanese Heart Journal, January, 1996, Volume 37, Number 1, 19-32	1, 2, 4-12, 35-50

第I欄 請求の範囲の一部の調査ができないときの意見 (第1ページの2の続き)

法第8条第3項 (PCT 17条(2)(a)) の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

1. ☒ 請求の範囲 22, 33, 51, 57, 66, 69, 76 は、この国際調査機関が調査をすることを要しない対象に係るものである。つまり、
請求の範囲 22, 33, 66, 69 の発明は「細胞のアポトーシスを抑制、促進または調節する方法」に関するものであるが、明細書にも記載されているように、これらはヒトの体内で治療を目的として実施されるものであるから、これらの発明は人の身体の治療による処置方法に該当する。また、請求の範囲 51, 57, 76 の発明は、「抗体と
2. ☐ 請求の範囲 _____ は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、
3. ☐ 請求の範囲 _____ は、従属請求の範囲であって PCT 規則 6.4(a) の第2文及び第3文の規定に従って記載されていない。

第II欄 発明の単一性が欠如しているときの意見 (第1ページの3の続き)

次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

国際出願における発明の単一性の要件 (PCT 規則 13.1) は、請求の範囲に記載された一群の発明の間に一又は二以上の同一又は対応する特別な技術的特徴を含む技術的關係があるときに限り、満たされるものであって、この「特別な技術的特徴」とは、請求の範囲に記載された各発明が全体として先行技術に対して行う貢献を明示する技術的特徴のことである (PCT 規則 13.2)。また、発明の単一性の要件の判断は、一群の発明が別個の請求の範囲に記載されているか単一の請求の範囲に択一的な形式によって記載されているかを考慮することなく行われる (PCT 規則 13.3)。

そこで、請求の範囲をみると、請求の範囲に記載された配列番号 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113

1. ☐ 出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求の範囲について作成した。
2. ☐ 追加調査手数料を要求するまでもなく、すべての調査可能な請求の範囲について調査することができたので、追加調査手数料の納付を求めなかった。
3. ☐ 出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったため、この国際調査報告は、手数料の納付のあった次の請求の範囲のみについて作成した。
4. ☒ 出願人が必要な追加調査手数料を期間内に納付しなかったため、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求の範囲について作成した。

請求の範囲中の配列番号 143 で表される塩基配列又は配列番号 144 で表されるアミノ酸配列に関連した発明

追加調査手数料の異議の申立てに関する注意

- ☐ 追加調査手数料の納付と共に出願人から異議申立てがあった。
☐ 追加調査手数料の納付と共に出願人から異議申立てがなかった。